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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 12:10:55 ; Search time 171 Seconds
(without alignments)
7697.915 Million cell updates/sec

Title: US-10-063-670-5
Perfect score: 2372
Sequence: 1 agcagggaatccggatgc.....ttaagcatttagaaactt 2372

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2372	100.0	2372	4	US-09-907-794A-200
2	2372	100.0	2372	4	US-09-905-125A-200
3	2372	100.0	2372	4	US-09-902-775A-200
4	2372	100.0	2404	4	US-09-833-381-849
5	2372	100.0	2404	4	US-09-833-381-853
6	2290.2	96.6	2313	2	US-08-892-880-1
7	1994	84.1	2029	4	US-09-232-160-13
8	603.6	25.4	1896	4	US-09-724-864-28
9	334	14.1	339	2	US-08-832-880-11
10	296.8	12.5	492	2	US-08-892-880-12
11	239	10.1	241	4	US-09-389-681-324
12	239	10.1	241	4	US-09-620-405B-324
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19	237	10.0	241	4	US-09-604-287A-323
20	237	10.0	241	4	US-08-834-759-323
21	226.2	9.5	239	2	US-08-892-880-14
22	191.4	8.1	466	2	US-08-892-880-13
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25	51.2	2.2	724	3	US-08-998-416-683
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27	50	2.1	50	4	US-09-905-125A-205

28	50	2.1	50	4	US-09-902-775A-205
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31	49.2	2.1	854	3	US-08-998-416-534
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33	48.4	2.0	640681	4	US-09-790-988-1
34	48.2	2.0	1587	4	US-09-010-147B-19
35	48.2	2.0	1720	4	US-09-148-545-53
36	46.6	2.0	3207	1	US-07-946-497-1
37	46.6	2.0	3207	1	US-08-483-322-1
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40	46	1.9	832	4	US-09-621-976-2813
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42	46	1.9	6113	4	US-10-204-708-13
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ALIGNMENTS

RESULT 1

US-09-907-794A-200
; Sequence 200, Application US/09907794A
; Patent No. 6635468

GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 200
;; LENGTH: 2372
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-907-794A-200

Query Match 100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AGCAGGAAATCCGGATGCTCCGTTATGAAGTGGAGCAGTGTGAGCCTCAACATA 60
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DB 61 GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC 120
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RESULT 2

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; Sequence 200, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Bacon, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
```

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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-905-125A-200

Query Match 100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCAGGGAAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAAGTGGAGCCTCAACATA 60
Db 1 AGCAGGGAAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAAGTGGAGCCTCAACATA 60
QY 61 GTTCCCAACTCTCCATCCGACTAGTTATAGCACTCTGCTCTATATACCAAGTGGC 120
Db 61 GTTCCCAACTCTCCATCCGACTAGTTATAGCACTCTGCTCTATATACCAAGTGGC 120
QY 121 CATCTGAGGTGTTTCCCTGCTCTGAAGGGGTAGGCAAGTGGCCAGGTGCTTCAGCCTG 180
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QY 181 GTGTTGCTTCTCACTTCCATCTGAGCAACAAGGCTCTCTGCTCAAGGCTCTTTGCGTGA 240
Db 181 GTGTTGCTTCTCACTTCCATCTGAGCAACAAGGCTCTCTGCTCAAGGCTCTTTGCGTGA 240
QY 241 GAAGAGCTTTCCATCCAGGTGTCAAGCAATTTATGGGATCACCTTGTGAGCAAAAAG 300
Db 241 GAAGAGCTTTCCATCCAGGTGTCAAGCAATTTATGGGATCACCTTGTGAGCAAAAAG 300
QY 301 GCGAACCAAGCAGCTGAATTTTACAGAGAGCTTAAGGAGGCTGTAGGCTGCTGGGACTAAGT 360
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Db 301 GCGAACACAGCAGCTGAATTTTCACAGAGCTAAGGAGGCCTGTAGGCTGTGGAGCTAAAGT 360
QY 361 TTGGCCGGCAGAGCAACAGCTTGAACACAGCTTGAAGCTAGCTTTGAACCTTGCAGCTAT 420
Db 361 TTGGCCGGCAGAGCAACAGCTTGAACACAGCTTGAAGCTAGCTTTGAACCTTGCAGCTAT 420
QY 421 GCCTGGGTGGAGATGGATTCCTGGTCACTCTAGGATTTAGCCCAACCCCAAGTGTGG 480
Db 421 GCCTGGGTGGAGATGGATTCCTGGTCACTCTAGGATTTAGCCCAACCCCAAGTGTGG 480
QY 481 AAAAATGGGTGGGTCTCTGATTTGGAAGTTCAGTCAGCCGACAGTTCGACGCTAT 540
Db 481 AAAAATGGGTGGGTCTCTGATTTGGAAGTTCAGTCAGCCGACAGTTCGACGCTAT 540
QY 541 TGTTCACACTCACTCTGATACCTTGGACTAACTCGTGATTCAGAAATATCACCAACCAA 600
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QY 1741 GCAGGACTGTAAACACACAGAGGCTCAAGGTTTTCTCTGAAACACATTTGAGTTGGAAT 1800
Db 1741 GCAGGACTGTAAACACACAGAGGCTCAAGGTTTTCTCTGAAACACATTTGAGTTGGAAT 1800
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGCTCTCTACACCTGCTGATATTTCTCT 1860
Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGCTCTCTACACCTGCTGATATTTCTCT 1860
QY 1861 AGGAATAATACCTTTTACAAGTAACAAAATAAATAAATAAATAAATAAATAAATAAATA 1920
Db 1861 AGGAATAATACCTTTTACAAGTAACAAAATAAATAAATAAATAAATAAATAAATAAATA 1920
QY 1921 GAGTACAGAAATGATTTACTAAGAGATTTACTCAGTAATTTGTTTAAAAAGTAAATAAA 1980
Db 1921 GAGTACAGAAATGATTTACTAAGAGATTTACTCAGTAATTTGTTTAAAAAGTAAATAAA 1980
QY 1981 TTCAACAAAACATTTGCTGAATAGTACTATATGTCAGTGTCTGCAAGGTATTACACTC 2040
Db 1981 TTCAACAAAACATTTGCTGAATAGTACTATATGTCAGTGTCTGCAAGGTATTACACTC 2040
QY 2041 TGTAATTTGAATTTATTTCTCAAAAATTTGACATAGTAGAAGCTATCTGGAGAGCTAT 2100
Db 2041 TGTAATTTGAATTTATTTCTCAAAAATTTGACATAGTAGAAGCTATCTGGAGAGCTAT 2100
QY 2101 TTTTTCAGTTTGTGATTTCTAGCTTATCTATCTTCCAAACTAATTTTATTTTGTCTGA 2160
Db 2101 TTTTTCAGTTTGTGATTTCTAGCTTATCTATCTTCCAAACTAATTTTATTTTGTCTGA 2160
QY 2161 GACTAATCTTATTTCTATTTCTTAATATGGCAACCATTAACCTTAATTTTATTTATTAAC 2220
Db 2161 GACTAATCTTATTTCTATTTCTTAATATGGCAACCATTAACCTTAATTTTATTTATTAAC 2220
QY 2221 ATACCTAAGAGTACATTTGTTTACCTTATATACCAAGACACATTTAAAAAGTGCATTA 2280
Db 2221 ATACCTAAGAGTACATTTGTTTACCTTATATATACCAAGACACATTTAAAAAGTGCATTA 2280
QY 2281 CAAATGTATCACTAGCCCTCTTTTCCAAAGAGAGGAGTGTAGAGATGAGAGATTT 2340
Db 2281 CAAATGTATCACTAGCCCTCTTTTCCAAAGAGAGGAGTGTAGAGATGAGAGATTT 2340
QY 2341 TGTGACAAAAAATTTAAAGCATTTAGAAAACTT 2372
Db 2341 TGTGACAAAAAATTTAAAGCATTTAGAAAACTT 2372

RESULT 3

US-09-775A-200
; Sequence 200, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

APPLICANT:	Ashkenazi, Avi	QY	1	AGCAGGGAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCTCAACATA	60
APPLICANT:	Botstein, David	Db	1	AGCAGGGAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCTCAACATA	60
APPLICANT:	Desnovers, Luc	QY	61	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCTCTCATATCACCAAGTGGC	120
APPLICANT:	Eaton, Dan L.	Db	61	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCTCTCATATCACCAAGTGGC	120
APPLICANT:	Ferrara, Napoleone	QY	121	CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGACAGATGGCCAGGTCCTTCAGCCTG	180
APPLICANT:	Filvaroff, Ellen	Db	121	CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGACAGATGGCCAGGTCCTTCAGCCTG	180
APPLICANT:	Fong, Sherman	QY	181	GTGTTGCTTCTCATTCCATCTGGACACAGAGGCTCCTGGTCCAAAGGCTCTTTGGGTGCA	240
APPLICANT:	Gao, Wei-Qiang	Db	181	GTGTTGCTTCTCATTCCATCTGGACACAGAGGCTCCTGGTCCAAAGGCTCTTTGGGTGCA	240
APPLICANT:	Gerber, Hanspeter	QY	241	GAAGAGCTTTCCATCCAGGTGTCATGCGAATATTGGGATCACCTTGTGAGCAAAAG	300
APPLICANT:	Gerritsen, Mary E.	Db	241	GAAGAGCTTTCCATCCAGGTGTCATGCGAATATTGGGATCACCTTGTGAGCAAAAG	300
APPLICANT:	Goddard, A.	QY	301	GGGAACACGACAGTGAATTTACAGAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGT	360
APPLICANT:	Godowski, Paul J.	Db	301	GGGAACACGACAGTGAATTTACAGAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGT	360
APPLICANT:	Grimaldi, Christopher J.	QY	361	TTGGCCGGCAAGGACCAAGTTGAAAAGCTTAGCTTTGAAAACCTTGCAGCTAT	420
APPLICANT:	Gurney, Austin L.	Db	361	TTGGCCGGCAAGGACCAAGTTGAAAAGCTTAGCTTTGAAAACCTTGCAGCTAT	420
APPLICANT:	Hillan, Kenneth, J.	QY	421	GGCTGGTTGGAGATGGATTTCGTGGTTCATCTAGGATTAGCCAAACCCCAAGTGGG	480
APPLICANT:	Hillan, Kenneth, J.	Db	421	GGCTGGTTGGAGATGGATTTCGTGGTTCATCTAGGATTAGCCAAACCCCAAGTGGG	480
APPLICANT:	Kl'avin, Ivar J.	QY	481	AAAAATGGGGTGGGTTGCTGCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTGAGCCCTAT	540
APPLICANT:	Kl'avin, Ivar J.	Db	481	AAAAATGGGGTGGGTTGCTGCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTGAGCCCTAT	540
APPLICANT:	Mather, Jennie P.	QY	541	TGTTTCAACTCATCTGATGATCTTGGACTAATCGTGATTCAGAAATTCACCAACCAAA	600
APPLICANT:	Mather, Jennie P.	Db	541	TGTTTCAACTCATCTGATGATCTTGGACTAATCGTGATTCAGAAATTCACCAACCAAA	600
APPLICANT:	Pan, James	QY	601	GATCCCATATTCACACTCAAACTGCAACACAAACAGAAATTTATTTGTCAGTGACAGT	660
APPLICANT:	Pan, James	Db	601	GATCCCATATTCACACTCAAACTGCAACACAAACAGAAATTTATTTGTCAGTGACAGT	660
APPLICANT:	Paoani, Nicholas F.	QY	661	ACTTACTCGGTGGCATCCCTTACTTCAATACCTGCCCCCTACTACTCTCTCTCTGCT	720
APPLICANT:	Paoani, Nicholas F.	Db	661	ACTTACTCGGTGGCATCCCTTACTTCAATACCTGCCCCCTACTACTCTCTCTCTGCT	720
APPLICANT:	Roy, Margaret Ann	QY	721	CCAGCTTCCACTTCTATTCCACGAGAAAAAATTTGATTTGTGTCTCAGAAATTTTATG	780
APPLICANT:	Roy, Margaret Ann	Db	721	CCAGCTTCCACTTCTATTCCACGAGAAAAAATTTGATTTGTGTCTCAGAAATTTTATG	780
APPLICANT:	Stewart, Timothy A.	QY	781	GAACTAGCACCATGCTCTACAGAACTGAACCAATTTGTTGAAATAAAGCAGATTCAG	840
APPLICANT:	Stewart, Timothy A.	Db	781	GAACTAGCACCATGCTCTACAGAACTGAACCAATTTGTTGAAATAAAGCAGATTCAG	840
APPLICANT:	Tomas, Daniel	QY	841	AATGAAGCTGCTGGGTTGGAGGTGTCCTGAGGTGTCCTGAGGTGTCCTGCTCTCTTC	900
APPLICANT:	Tomas, Daniel	Db	841	AATGAAGCTGCTGGGTTGGAGGTGTCCTGAGGTGTCCTGAGGTGTCCTGCTCTCTTC	900
APPLICANT:	Williams, P. Mickey	QY	901	TTTGGTGTGCTGAGCTGCTGCTGATTTGCTATGTCTCAAAAGGTATGTGAAGGCTTCCCT	960
APPLICANT:	Williams, P. Mickey	Db	901	TTTGGTGTGCTGAGCTGCTGCTGATTTGCTATGTCTCAAAAGGTATGTGAAGGCTTCCCT	960
APPLICANT:	Wood, William I.	QY	961	TTTACAAAACAGAAATCAGCAGAAAGGAAATGATCGAAACCAAACTAGTAAAGGAGGAG	1020
APPLICANT:	Wood, William I.	Db	961	TTTACAAAACAGAAATCAGCAGAAAGGAAATGATCGAAACCAAACTAGTAAAGGAGGAG	1020
APPLICANT:	Wood, William I.	QY	1021	GCAATGATAGCAACCTTATGAGGATCAAGAGAACTGATTAAGGAGGAGGAGTCC	1080
APPLICANT:	Wood, William I.	Db	1021	GCAATGATAGCAACCTTATGAGGATCAAGAGAACTGATTAAGGAGGAGGAGTCC	1080

Query Match 100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1081 AAGAGTCAAGCAAACTACCGTGCATGCGTGAAGCTGAAGTTAGATGAGACAGAAA 1140
QY 1141 TGAGGAGACACACCTGAGCGTGTCTTCTCATGCTCCCTTACCTGCCGCCAGCTGGGAA 1200
Db 1141 TGAGGAGACACACCTGAGCGTGTCTTCTCATGCTCCCTTACCTGCCGCCAGCTGGGAA 1200
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Db 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTTGGTTCTTAACCTGAATCAGC 1260
QY 1261 TCAGGACTGCCATTCGACTATGGAGTGACCAAAAGAGAAAGTCCACCCCTTGGTTCTTAACCTGAATCAGC 1320
Db 1261 TCAGGACTGCCATTCGACTATGGAGTGACCAAAAGAGAAAGTCCACCCCTTGGTTCTTAACCTGAATCAGC 1320
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Db 1321 CCTGCTCGATCTATCTCTCTACCTCCAAAGCTTCCCAAGCTTCCCAAGCTTCCAGCTGGCTAT 1380
QY 1381 GTCTTAATAATATCCACTGGGAGAAAGGAGTTTGGCAAAGTGCAAGGACCTAAACATC 1440
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QY 1441 TCATCAGTATCCAGTGGTAAAGGCCCTCTGGCTGTCTGAGGCTAGTGGGTGAAGC 1500
Db 1441 TCATCAGTATCCAGTGGTAAAGGCCCTCTGGCTGTCTGAGGCTAGTGGGTGAAGC 1500
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Db 1501 CAAGGAGTCACTGAGACCAAGCTTCTCTACTGATTCGCGAGCTCAGACCTTCTTCA 1560
QY 1561 GCTCTGAAGAGAAACAGTATCCACCTGACATGTCTCTCTGAGCCGGTGAAGCAAA 1620
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Db 1681 TCTCTGAAGCTAAAATAAAGAAATAGAAACAGGCTGAGGATACGACAGTACACTGCA 1740
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Db 1741 GCAGGACTGTAAACACAGACAGGCTCAAGTGTCTCTGTAACACATTCAGTTGGAAT 1800
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Db 1801 CACTGTTTAGAACACACACTTACTTCTGCTCTCTACCACTGCTGATTTCTCT 1860
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Db 1861 AGAAATATACTTTTCAAGTAACAAATAAATAAATCTTATAATTTCTATTTTATCT 1920
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Db 1921 GAGTTACAGAAATGATTAAGGAAGATTAAGTAAATTTGTTTAAAAAGTAATAAAA 1980
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Db 1981 TTCAACAAACATTTGCTGATAGTACTATATCTCAAGTCTGTCGAGGATTTACACTC 2040
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QY 2101 TTTTTCAGTTTGTATTTCTAGCTTATCTATCTCCAAACTAATTTTATTTTCTGTA 2160
Db 2101 TTTTTCAGTTTGTATTTCTAGCTTATCTATCTCCAAACTAATTTTATTTTCTGTA 2160
QY 2161 GACTAATCTTATTTCTTAATATGCAACCAATTAACCTTAATTTATTTATTAAC 2220
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Db 2161 GACTAATCTTATTTCTTAATATGCAACCAATTAACCTTAATTTATTTATTAAC 2220
QY 2221 ATACCTAAGAAGTACATTTGTTACCTCTATATACAAAGACATTTTAAAGTGCCATTA 2280
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QY 2281 CAATGTATCACTAGCCCTCTTTTCCAAAGAGGAGCTGAGAGATGCAAAATATT 2340
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Db 2341 TGTGACAAAAAATTAAGCAATTTAGAAAACTT 2372
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RESULT 4
US-09-833-381-849
; Sequence 849, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 849
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-849

Query Match 100.0%; Score 2372; DB 4; Length 2404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 31 AGCAGGGAATCCGGATGTCTCGTTATGAAGTGGAGCAGTGTGAGCCTCAACATA 90
QY 61 GTTCAGAACTCTCCATCCGAGTGTATTTAGCANTCTGCCTCTCATATACCAGTGC 120
Db 91 GTTCAGAACTCTCCATCCGAGTGTATTTAGCANTCTGCCTCTCATATACCAGTGC 150
QY 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGTCTTCAGCCTG 180
Db 151 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGTCTTCAGCCTG 210
QY 181 GTGTTGCTTCTCACTTCCATCTGACCAACAGGCTCTGTGTCAGAGCTCTTTGCGTGCA 240
Db 211 GTGTTGCTTCTCACTTCCATCTGACCAACAGGCTCTGTGTCAGAGCTCTTTGCGTGCA 270
QY 241 GAAGAGCTTTCCATCCAGTGTCTATGCAGAAATTTATGGGATCACCTTGTGAGCAAAAG 300
Db 271 GAAGAGCTTTCCATCCAGTGTCTATGCAGAAATTTATGGGATCACCTTGTGAGCAAAAG 330
QY 301 GCAGAACAGCAGCTGAATTTACAGAGCTTAAGAGGCCCTGTAGGCTGTGGGACTAAGT 360
Db 331 GCAGAACAGCAGCTGAATTTACAGAGCTTAAGAGGCCCTGTAGGCTGTGGGACTAAGT 390
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Db 391 TTGGCCGGCAAGCAGCAAGTTGAAACAGCTTGAAGAGCTAGCTTTGAACTTGCAGCTAT 450
QY 421 GGCTGGTTGGAGATGGATTCTGTTGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG 480
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QY 481 AAAAAATGGGGTGGGTGTCCTGATTTTGGAAAGTTTCCAGTGGCCGACAGATTTGAGCCTAT 540
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Db 631 GATCCATATTCAACACTCAAACTCGAACAACAAACAAAGATTTATTTGTCAGTACAGAT 690
QY 661 ACCTACTCGGTGGATCCCTTACTCTCAATACCTGCCCCCTACTACTCTCTCTGCT 720
Db 691 ACCTACTCGGTGGATCCCTTACTCTCAATACCTGCCCCCTACTACTCTCTCTGCT 750
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Db 751 CCAGCTTCCACTCTTATCCACGGAGAAAATTTGATTTGTCACAGAAATTTTATG 810
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Db 811 GAAACTAGCAACCATGTCACAGAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAG 870
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Db 1531 CAAGGAGTCACTGAGACAAGAGCTTCTCTACTGATTCGGCAGCTCAGACCTTCTTCA 1590
QY 1561 GCTCTGAAGAGAAACAGTATCCACTGACATGCTCTCTGAGCCCGGTAAAGCAAA 1620
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Db 1591 GCTCTGAAAGAGAAACACGTTATCCACCTGACATGCTCTGTGAGCCCGGTAAAGCAAA 1650
QY 1621 AGAATGGCAGAAAAGTTTGTAGCCCTGAAAGCCATGAGATTCTCATAACTTGAGACTTAA 1680
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Db 1711 TCTCTGTAAGCTTAAATATAAATAAGAAATAGAAACAAAGGCTGAGGATACGACAGTAC 1770
QY 1741 GCAGGACTGTAAACACACAGACAGGCTGAAAGTGTCTCTGAAACACATTGAGTTGGAT 1800
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Db 1831 CACTCTTTAGAACACACACACTTACTTTTCTGTTGCTCTACCACTGCTGATATTTCTCT 1890
QY 1861 AGGAATATATCTTTTACAAAGTAACAAAAATAAAAACTCTTATFAAATTTCTATTTTATCT 1920
Db 1891 AGGAATATATCTTTTACAAAGTAACAAAAATAAAAACTCTTATFAAATTTCTATTTTATCT 1950
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Db 1951 GAGTTACAGAAATGATTAAGGAGGATTAAGGAGGATTAAGGAGGATTAAGGAGGATTA 2010
QY 1981 TTTCAACAAACATTTGCTGAATAGTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040
Db 2011 TTTCAACAAACATTTGCTGAATAGTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2070
QY 2041 TGTAAATGTAATATTTTCTCAAAAAATTTGCAATAGTAGAAGCGTATCTGGGAAGCTAT 2100
Db 2071 TGTAAATGTAATATTTTCTCAAAAAATTTGCAATAGTAGAAGCGTATCTGGGAAGCTAT 2130
QY 2101 TTTTTCAGTTTGTATTTCTAGCTTATCTACTTCCAACTAAATTTTATTTTCTGCTGA 2160
Db 2131 TTTTTCAGTTTGTATTTCTAGCTTATCTACTTCCAACTAAATTTTATTTTCTGCTGA 2190
QY 2161 GACTAATCTTATTTCTATTTCTTAAATGCGCAACCAATATAAACCCTTAAATTTATTAAC 2220
Db 2191 GACTAATCTTATTTCTTAAATGCGCAACCAATATAAACCCTTAAATTTATTAAC 2250
QY 2221 ATACCTTAAGAGTACATTTGTTACCTCTATATATCAAAAGCAGACATTTTAAAGTCCCAATA 2280
Db 2251 ATACCTTAAGAGTACATTTGTTACCTCTATATATCAAAAGCAGACATTTTAAAGTCCCAATA 2310
QY 2281 CAAATGTATCACTAGCCCTCTTTTCCAAAGAGGAGCTGAGAGATCGAGAAATATT 2340
Db 2311 CAAATGTATCACTAGCCCTCTTTTCCAAAGAGGAGCTGAGAGATCGAGAAATATT 2370
QY 2341 TGTGACAAAAATTAAGCAATTTAGAAAACTT 2372
Db 2371 TGTGACAAAAATTAAGCAATTTAGAAAACTT 2402

RESULT 5

US-09-833-381-853
; Sequence 853, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 853
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-833-381-853

Query Match				100.0%; Score 2372; DB 4; Length 2404;			
Best Local Similarity				100.0%; Pred. No. 0;			
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
QY	1	AGCAGGAAATCCGGATGTCCTGGTTATGAAGTGGAGCAGTGAAGTGGAGCCCTCAACATA	60				
DB	31	AGCAGGAAATCCGGATGTCCTGGTTATGAAGTGGAGCAGTGAAGTGGAGCCCTCAACATA	90				
QY	61	GTTCAGAACTCTCCATCCGACTAGTTATTTGAGCATCTGCCTCTCATATACACAGTGGC	120				
DB	91	GTTCAGAACTCTCCATCCGACTAGTTATTTGAGCATCTGCCTCTCATATACACAGTGGC	150				
QY	121	CATCTGAGTGTTCCTCCGTCTCAAGGGGTAGGCACGATGGCCAGGTCTTACGCCCTG	180				
DB	151	CATCTGAGTGTTCCTCCGTCTCAAGGGGTAGGCACGATGGCCAGGTCTTACGCCCTG	210				
QY	181	GTGTTGCTTCTCATCTCCATCTGGACACGAGGCTCTGGTCCAAAGGCTCTTTGGGTGCA	240				
DB	211	GTGTTGCTTCTCATCTCCATCTGGACACGAGGCTCTGGTCCAAAGGCTCTTTGGGTGCA	270				
QY	241	GAAGAGCTTTCCATCCAGTGTCAATGAGAAATTTAGGGGATCAACCCCTTGTGAGCAAAAG	300				
DB	271	GAAGAGCTTTCCATCCAGTGTCAATGAGAAATTTAGGGGATCAACCCCTTGTGAGCAAAAG	330				
QY	301	CGCAACACAGCAGCTGAATTTACAGAACTAAGAGGCTCTGAGGCTCTGGGACTAAGT	360				
DB	331	CGCAACACAGCAGCTGAATTTACAGAACTAAGAGGCTCTGAGGCTCTGGGACTAAGT	390				
QY	361	TTGGCCGGCAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTAT	420				
DB	391	TTGGCCGGCAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTAT	450				
QY	421	GGCTGGTTGAGATGATTCGCTGATCTAGGATTTAGCCCAACCCCAAGTGGG	480				
DB	451	GGCTGGTTGAGATGATTCGCTGATCTAGGATTTAGCCCAACCCCAAGTGGG	510				
QY	481	AAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGGAGCCTAT	540				
DB	511	AAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGGAGCCTAT	570				
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QY	601	GATCCCATTTCAACACTCAAACTGCAACACAAACAGAAATTTATGTCAGTGACAGT	660				
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DB	691	ACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCCCTACTACTCTCCTCTGCT	750				
QY	721	CCAGCTTCCACTTCTATTTCCAGGAGAAAAAATGATTTGTTGTTGTCACAGAAATTTATG	780				
DB	751	CCAGCTTCCACTTCTATTTCCAGGAGAAAAAATGATTTGTTGTTGTCACAGAAATTTATG	810				
QY	781	GAACCTAGACCACTGTCTACAGAACTGAACCAATTTGTTGAAATTAAGCAGCAATTTCAAG	840				
DB	811	GAACCTAGACCACTGTCTACAGAACTGAACCAATTTGTTGAAATTAAGCAGCAATTTCAAG	870				
QY	841	AATGAGCTCTGGTTGGAGTGTCCCAAGGCTCTGCTAGTGTCTCTCCTCTTC	900				
DB	871	AATGAGCTCTGGTTGGAGTGTCCCAAGGCTCTGCTAGTGTCTCTCCTCTTC	930				
QY	901	TTTGGTGTCTGAGTGTCTGATTTGCTATGTTCAAAAGGATTTGTTGAGGCTTCCCT	960				
DB	931	TTTGGTGTCTGAGTGTCTGATTTGCTATGTTCAAAAGGATTTGTTGAGGCTTCCCT	990				
QY	961	TTTCAAAACAGAAATCAGCAGAGGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAG	1020				
DB	991	TTTCAAAACAGAAATCAGCAGAGGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAG	1050				

QY	1021	GCCATGATAGCAACCCCTAATGAGCAATCAAGAAACCTGATAAAACCCAGAGAGTCC	1080
DB	1051	GCCATGATAGCAACCCCTAATGAGCAATCAAGAAACCTGATAAAACCCAGAGAGTCC	1110
QY	1081	AAGAGTCCAAAGCAAACTACCGTGCATGCCCTGGAAGCTGAAGTTTATGATGAGACAGAAA	1140
DB	1111	AAGAGTCCAAAGCAAACTACCGTGCATGCCCTGGAAGCTGAAGTTTATGATGAGACAGAAA	1170
QY	1141	TGAGAGACACACCTGAGGCTGTTCTTTCATGCTCTCTTACCTTGCCTTCTTAACTGGAATCAGC	1200
DB	1171	TGAGAGACACACCTGAGGCTGTTCTTTCATGCTCTCTTACCTTGCCTTCTTAACTGGAATCAGC	1230
QY	1201	ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTTGGTTCCTTAACTGGAATCAGC	1260
DB	1231	ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTTGGTTCCTTAACTGGAATCAGC	1290
QY	1261	TCAGGACTGCCATTTGGACTATGGAGTGACCAAGAGAAATGCCCTTCTTAACTGGAATCAGC	1320
DB	1291	TCAGGACTGCCATTTGGACTATGGAGTGACCAAGAGAAATGCCCTTCTTAACTGGAATCAGC	1350
QY	1321	CCTGCTGGATCTCTATCTCTCTTACCTTCAAAAGCTTCCACCGGCTTCTAGCCTGGCTAT	1380
DB	1351	CCTGCTGGATCTCTATCTCTCTTACCTTCAAAAGCTTCCACCGGCTTCTAGCCTGGCTAT	1410
QY	1381	GTCTCTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAGGACCTTAAACATC	1440
DB	1411	GTCTCTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAGGACCTTAAACATC	1470
QY	1441	TCATCAGTATCCAGTGGTAAAAAGGCTTCTGAGGCTGCTGAGGCTAGGTGGTGGTAAAAAGC	1500
DB	1471	TCATCAGTATCCAGTGGTAAAAAGGCTTCTGAGGCTGCTGAGGCTAGGTGGTGGTAAAAAGC	1530
QY	1501	CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTTCCGAGCTGACACCTTCTTCA	1560
DB	1531	CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTTCCGAGCTGACACCTTCTTCA	1590
QY	1561	GCTCTGAAAGAGAAACACGATATCCCACTGACATGCTCTGAGCCCGGTAAAGACAAA	1620
DB	1591	GCTCTGAAAGAGAAACACGATATCCCACTGACATGCTCTGAGCCCGGTAAAGACAAA	1650
QY	1621	AGAAATGCGAGAAAGTTTAGCCCTGAAAGCCATGGAGATTTCTATACTTGAGACCTAA	1680
DB	1651	AGAAATGCGAGAAAGTTTAGCCCTGAAAGCCATGGAGATTTCTATACTTGAGACCTAA	1710
QY	1681	TCTCTGTAAGCTTAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACTGTCA	1740
DB	1711	TCTCTGTAAGCTTAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACTGTCA	1770
QY	1741	GCAGGACTCTTAAACACAGACAGGCTCAAAAGTGTCTCTGACACATTTGAGTGGAAAT	1800
DB	1771	GCAGGACTCTTAAACACAGACAGGCTCAAAAGTGTCTCTGACACATTTGAGTGGAAAT	1830
QY	1801	CACCTGTTAGAACACACACTTTACTTTTCTGCTCTCTACCACTGCTGATTTTCTCT	1860
DB	1831	CACCTGTTAGAACACACACTTTACTTTTCTGCTCTCTACCACTGCTGATTTTCTCT	1890
QY	1861	AGGAATATATCTTTTCAAGTAAACAAATAAATACTCTTATAAATTTCTATTTTATCT	1920
DB	1891	AGGAATATATCTTTTCAAGTAAACAAATAAATACTCTTATAAATTTCTATTTTATCT	1950
QY	1921	GAGTTACAGAAATGATTTACTTAAGGAAGATTTACTCAGTAAATTTCTTAAAGTAATAAAA	1980
DB	1951	GAGTTACAGAAATGATTTACTTAAGGAAGATTTACTCAGTAAATTTCTTAAAGTAATAAAA	2010
QY	1981	TTCAACAAACATTTGCTGTAATAGTACTATATCTCAAGTCTGTGCAAGGATTTTACATC	2040
DB	2011	TTCAACAAACATTTGCTGTAATAGTACTATATCTCAAGTCTGTGCAAGGATTTTACATC	2070
QY	2041	TGTAATTTGAAATTTATTTCTCTCAAAATTTGCACATAGTAGAACGCTATCTGGGAGCTAT	2100
DB	2071	TGTAATTTGAAATTTATTTCTCTCAAAATTTGCACATAGTAGAACGCTATCTGGGAGCTAT	2130

1095 AACTACCGTGGATGCGCTGGAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACC 1154
Db |||||
1026 AACTACCGTGGATGCGCTGGAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACC 1085
Qy |||||
1155 TGAGGCTGGTTCTTTTCAATGCTCCCTTACCTGCCCCAGCTGGGAAATCAAAAGGGCAA 1214
Db |||||
1086 TGAGGCTGGTTCTTTTCAATGCTCCCTTACCTGCCCCAGCTGGGAAATCAAAAGGGCAA 1145
Qy |||||
1215 AGRACCAAGAGAAAGTCCACCTTGGTTCCTTACCTGGAATCAGCTCAGACTGCCATT 1274
Db |||||
1146 AGRACCAAGAGAAAGTCCACCTTGGTTCCTTACCTGGAATCAGCTCAGACTGCCATT 1205
Qy |||||
1275 GGACTATGAGCTGACCAAGAGAAATGCCCTTCTCTTATTGTAAACCTGTCTGATCCT 1334
Db |||||
1206 GGACTATGAGCTGACCAAGAGAAATGCCCTTCTCTTATTGTAAACCTGTCTGATCCT 1265
Qy |||||
1335 ATCTCTTACCTCAAAGCTTCCACGCGCTTCTAGCTGGCTATGCTCTTAATAATC 1394
Db |||||
1266 ATCTCTTACCTCAAAGCTTCCACGCGCTTCTAGCTGGCTATGCTCTTAATAATC 1325
Qy |||||
1395 CCCTGGGAGAAAGAGTTTTCGAAAGTGCAGGACCTTAAACATCTCATCAGTATCCAG 1454
Db |||||
1326 CCCTGGGAGAAAGAGTTTTCGAAAGTGCAGGACCTTAAACATCTCATCAGTATCCAG 1385
Qy |||||
1455 TGGTAAAAAGGCTTCTGAGCTGTCTGAGGCTAGTGGTTGAAAGCCCAAGAGTCACTGA 1514
Db |||||
1386 TGGTAAAAAGGCTTCTGAGCTGTCTGAGGCTAGTGGTTGAAAGCCCAAGAGTCACTGA 1445
Qy |||||
1515 GACCAAGGCTTCTACTGATTCGGAGCTCAGACCCCTTCTTCAAGCTCTGAAAGAGAA 1574
Db |||||
1446 GACCAAGGCTTCTACTGATTCGGAGCTCAGACCCCTTCTTCAAGCTCTGAAAGAGAA 1505
Qy |||||
1575 ACAGTATCCACCTGACATGCTCTCTGACCGGTAAAGCAAAAGTGGCAGAAA 1634
Db |||||
1506 ACAGTATCCACCTGACATGCTCTCTGACCGGTAAAGCAAAAGTGGCAGAAA 1565
Qy |||||
1635 GTTTAGCCCTTGAAGCCATGAGATCTCTATACTTGAACCTTAATCTCTGTAAAGCTA 1694
Db |||||
1566 GTTTAGCCCTTGAAGCCATGAGATCTCTATACTTGAACCTTAATCTCTGTAAAGCTA 1625
Qy |||||
1695 AAATAAGAAATAGAACAGCTGAGATACGACATGCTCAGCAGGAGCTGTAA 1754
Db |||||
1626 AAATAAGAAATAGAACAGCTGAGATACGACATGCTCAGCAGGAGCTGTAA 1685
Qy |||||
1755 CACAGACAGGCTCAAGGTTTTCTCTGAACACATGAGTTGGAATCACTGTTAGACA 1814
Db |||||
1686 CACAGACAGGCTCAAGGTTTTCTCTGAACACATGAGTTGGAATCACTGTTAGACA 1745
Qy |||||
1815 CACACACTTACTTTTCTGPTCTCTACACCTGCTGATATTTTCTAGGAAATATACCTT 1874
Db |||||
1746 CACACACTTACTTTTCTGPTCTCTACACCTGCTGATATTTTCTAGGAAATATACCTT 1805
Qy |||||
1875 TACAAGTAAACAAATATAAACTCTTATAATTTCTATTTTTATCTGAGTTACGAAATG 1934
Db |||||
1806 TACAAGTAAACAAATATAAACTCTTATAATTTCTATTTTTATCTGAGTTACGAAATG 1865
Qy |||||
1935 ATTAAGGAGGATTTACTCAGTAAATTTGTTTAAAAAGTATAAAATCAACAACATTT 1994
Db |||||
1866 ATTAAGGAGGATTTACTCAGTAAATTTGTTTAAAAAGTATAAAATCAACAACATTT 1925
Qy |||||
1995 GCTGAATAGCTTACTATATGTCAGTGTGTCAGAGGTATTACACTCTGTAAATGAATAT 2054
Db |||||
1926 GCTGAATAGCTTACTATATGTCAGTGTGTCAGAGGTATTACACTCTGTAAATGAATAT 1985
Qy |||||
2055 ATTCTCAAATAAATGACATAGTAGAAGCGTATCTGGGAAGCTATTTTTTCAGTTTTG 2114
Db |||||
1986 ATTCTCAAATAAATGACATAGTAGAAGCGTATCTGGGAAGCTATTTTTTCAGTTTTG 2045
Qy |||||
2115 ATATTCTAGCTTATCTACTTTCCAAACTAAATTTTTTATTTTGGCTGAGACTAATCTTATC 2174
Db |||||
2046 ATATTCTAGCTTATCTACTTTCCAAACTAAATTTTTTATTTTGGCTGAGACTAATCTTATC 2105

2175 ATTTTCTTAATATGGCAACCACTTATACCTTAATTTATTATTATTAACATACCTTAAGAATG 2234
Db |||||
2106 ATTTTCTTAATATGGCAACCACTTATACCTTAATTTATTATTATTAACATACCTTAAGAATG 2165
Qy |||||
2235 CATTTGTACCTCTATATACCAAGACATTTTAAAAAGTGCATTAACAAATGTATCACTA 2294
Db |||||
2166 CATTTGTACCTCTATATACCAAGACATTTTAAAAAGTGCATTAACAAATGTATCACTA 2225
Qy |||||
2295 GCCCTCCTTTTCCAAACAAGAGGAGCTGAGAGATGCAGAAATATTTCTGACAAAAAAT 2354
Db |||||
2226 GCCCTCCTTTTCCAAACAAGAGGAGCTGAGAGATGCAGAAATATTTCTGACAAAAAAT 2285
Qy |||||
2355 AAAGCAATTGAAAA 2369
Db |||||
2286 AAAGCAATTGAAAA 2300

RESULT 7

US-09-232-160-13
; Sequence 13, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James G. Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232.160
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 2029
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 3044710
US-09-232-160-13

Query Match 84.1%; Score 1994; DB 4; Length 2029;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AGCAGGGAATCCGGATCTCTCGGTTATGAGTGGAGCAGTGAGTGTCAGCCTCAACATA 60
Db 24 AGCAGGGAATCCGGATCTCTCGGTTATGAAAGTGGAGCAGTGAGTGTCAGCCTCAACATA 83
Qy 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC 120
Db 84 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC 143
Qy 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTGAGCAGATGGCCAGGTGTTCCAGCTG 180
Db 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTGAGCAGATGGCCAGGTGTTCCAGCTG 203
Qy 181 GTGTGCTTCTCAGTCTCCATCTGACACGAGGCTCTGGTCCAGGCTCTTTGCGTGCA 240
Db 204 GTGTGCTTCTCAGTCTCCATCTGACACGAGGCTCTGGTCCAGGCTCTTTGCGTGCA 263
Qy 241 GAAGAGCTTTTCCATCCAGGTGTCATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG 300
Db 264 GAAGAGCTTTTCCATCCAGGTGTCATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG 323
Qy 301 GCGAACACGAGCTGAATTTACAGAGCTTAAGAGGCTGTAGGCTGTGGGACTAAGT 360
Db 324 GCGAACACGAGCTGAATTTACAGAGCTTAAGAGGCTGTAGGCTGTGGGACTAAGT 383
Qy 361 TTGCGCGGAGGACCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTGAAACCTTTGAGCTAT 420
Db 384 TTGCGCGGAGGACCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTGAAACCTTTGAGCTAT 443

QY 421 GGCTGGGTTGGAGATGGATTCTGTGTGATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGG 480
DB 444 GGCTGGGTTGGAGATGGATTCTGTGTGATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGG 503
QY 481 AAAAATGGGTTGGGTTGCTGATTTGGGAAGGTTCCAGTGGAGCCGACAGTTTCAGCCTAT 540
DB 504 AAAAATGGGTTGGGTTGCTGATTTGGGAAGGTTCCAGTGGAGCCGACAGTTTCAGCCTAT 563
QY 541 TGTTCACACTCATCTGATCTATGACTAATCGTGCATTTCCAGAAATATATCAACCAAAA 600
DB 564 TGTTCACACTCATCTGATCTATGACTAATCGTGCATTTCCAGAAATATATCAACCAAAA 623
QY 601 GATCCATATTTCAACACTCAAACTGCAACACAACTGTTGTTGAAATTAAGACAGATTCAAG 660
DB 624 GATCCATATTTCAACACTCAAACTGCAACACAACTGTTGTTGAAATTAAGACAGATTCAAG 683
QY 661 ACCTACTCGTGGGATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCTCTGCT 720
DB 684 ACCTACTCGTGGGATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCTCTGCT 743
QY 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTGCACAGAGTTTATG 780
DB 744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTGCACAGAGTTTATG 803
QY 781 GAAACTAGACCATGCTACAGAACTGAACCACTTTGTTGAAATTAAGACAGATTCAAG 840
DB 804 GAAACTAGACCATGCTACAGAACTGAACCACTTTGTTGAAATTAAGACAGATTCAAG 863
QY 841 AATGAAGCTGCTGGGTTTGGAGGTGCCCCACGGCTCTGTAGTGTGCTCTCTCTCTTC 900
DB 864 AATGAAGCTGCTGGGTTTGGAGGTGCCCCACGGCTCTGTAGTGTGCTCTCTCTTC 923
QY 901 TTTGTGTGCTGAGCTGGTCTTGGATTTTGTCTATGTCAAAAGTATGTGAAGGCTTCCCT 960
DB 924 TTTGTGTGCTGAGCTGGTCTTGGATTTTGTCTATGTCAAAAGTATGTGAAGGCTTCCCT 983
QY 961 TTTTCAAAACAGATCAGCAGAGGAAGTATGTCGAAACCAAGTATGAAAGGAGGAG 1020
DB 984 TTTTCAAAACAGATCAGCAGAGGAAGTATGTCGAAACCAAGTATGAAAGGAGGAG 1043
QY 1021 GCCAATGATAGCAACCTTATAGAGGATCAAGAAAACTGATAAAAAACCCAGAAAGTCC 1080
DB 1044 GCCAATGATAGCAACCTTATAGAGGATCAAGAAAACTGATAAAAAACCCAGAAAGTCC 1103
QY 1081 AAGAGTCCAAAGCAAACTACCGTGCAGTCCCTGGAGCTGAAATTTAGATGACAGAAA 1140
DB 1104 AAGAGTCCAAAGCAAACTACCGTGCAGTCCCTGGAGCTGAAATTTAGATGACAGAAA 1163
QY 1141 TGAGGAGACACACTGAGGTGGTCTTCTTATGCTCTTACCTGCTTACCTGCCCGCTGGGAA 1200
DB 1164 TGAGGAGACACACTGAGGTGGTCTTCTTATGCTCTTACCTGCTTACCTGCCCGCTGGGAA 1223
QY 1201 ATCAAAAGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCTCTAACTGGAATCAGC 1260
DB 1224 ATCAAAAGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCTTAACTGGAATCAGC 1283
QY 1261 TCAGGACTGCCATTGGAATGAGTGACAAAGAGAAATGCCCTTCTCTTATTTGAAC 1320
DB 1284 TCAGGACTGCCATTGGAATGAGTGACAAAGAGAAATGCCCTTCTCTTATTTGAAC 1343
QY 1321 CCTGTCTGGATCCTATCCTCTACCTCAAGCTTCCAGGGCTTCTAGCCTGGCTAT 1380
DB 1344 CCTGTCTGGATCCTATCCTCTACCTCAAGCTTCCAGGGCTTCTAGCCTGGCTAT 1403
QY 1381 GTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCAGAAAGTCAAGGACTCAAAAATC 1440
DB 1404 GTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCAGAAAGTCAAGGACTCAAAAATC 1463
QY 1441 TCATCAGTATCCAGTGTGTAAGAGGCTCTCTGCTGTCTGAGGCTAGGTGGGTTGAAAGC 1500
DB 1464 TCATCAGTATCCAGTGTGTAAGAGGCTCTCTGCTGTCTGAGGCTAGGTGGGTTGAAAGC 1523
QY 1501 CAAGGAGTCTAGACCAAGGCTTTCTCTACTGATTTCCGAGCTCAGACCCCTTCTTCA 1560

DB 1524 CAAGGAGTCTAGACCAAGGCTTTCTACTGATTCOGCAGCTCAGACCCCTTCTTCA 1583
QY 1561 GCTCTGAAAGAGAAAACAGTATCCCACTGACATGCTCTTGAGCCCGGTAAGAGCAAA 1620
DB 1584 GCTCTGAAAGAGAAAACAGTATCCCACTGACATGCTCTTGAGCCCGGTAAGAGCAAA 1643
QY 1621 AGAATGGCAGAAAAGTTTGTAGCCCTGAAAGCCATGAGATTCCTATAACTTCGAGACCTAA 1680
DB 1644 AGAATGGCAGAAAAGTTTGTAGCCCTGAAAGCCATGAGATTCCTATAACTTCGAGACCTAA 1703
QY 1681 TCTCTGTAAAGCTAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACCTGTCA 1740
DB 1704 TCTCTGTAAAGCTAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACCTGTCA 1763
QY 1741 GAGGAGCTGTAAACACAGACAGGGTCAAAAGTGTCTCTGAAACACATTTGAGTTGGAAT 1800
DB 1764 GAGGAGCTGTAAACACAGACAGGGTCAAAAGTGTCTCTGAAACACATTTGAGTTGGAAT 1823
QY 1801 CACTGTTTAGACACACACACTTACTTTTTCTGGTCTCTPACCACCTGCTGATTTTTCTCT 1860
DB 1824 CACTGTTTAGACACACACACTTACTTTTTCTGGTCTCTPACCACCTGCTGATTTTTCTCT 1883
QY 1861 AGGAATATATCTTTTACAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTTTATCT 1920
DB 1884 AGGAATATATCTTTTACAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTTTATCT 1943
QY 1921 GAGTTACAGAAATGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGG 1980
DB 1944 GAGTTACAGAAATGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGGATTAAGAGG 2003
QY 1981 TTTCAACAAACATTTGCTGAATA 2002
DB 2004 TTTCAACAAACATTTAAAAAAA 2025

RESULT 8

US-09-724-864-28
; Sequence 28, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.105001
; CURRENT APPLICATION NUMBER: US/09/724,864
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Mouse
US-09-724-864-28

Query Match 25.4%; Score 603.6; DB 4; Length 1896;
Best Local Similarity 76.2%; Pred. No. 2.3e-162;
Matches 786; Conservative 0; Mismatches 234; Indels 12; Gaps 3;
QY 140 GCTCTGAAGGGTAGGACAGATGCCAGGTGCTTCAAGGCTCTTTGGGTGCAGAGAGCTTTCCATCCAGG 199
DB 42 GCCCCGGAGGATCTGCACAATGCTCCAGCACACTAGCTGGTGTACTCTCGCTCTTA 101
QY 200 TCTGGACACAGAGCTCTTGGTCCAAAGGCTCTTTGGGTGCAGAGAGCTTTCCATCCAGG 259
DB 102 TTTGGACCACTAGCACCAGTCCAGGTGCCACCTCGTGCAGAGCTTTCCAT---TT 158
QY 260 TGTCTGACAGATTTATGGGATCACCTTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAAT 319
DB 159 CTACATGCAATCATGGGGTTGCCCTTTGTGGGAGAAAACAAAAACCCACAGATGAAT 218

Qy 320 TCACAGAGCTAAGGAGGCTGTAGGCTGTGGACTAAGTTGGCCGCGCAAGGACCAAG 379
Db 219 TCACAGAGGCAACGAGGCTGTAGGCTGTGGACTAAGTTGGCCGCGCAAGGACCAAG 278
Qy 380 TTGAACAGCCTTGAAGCTAGCTTTGAACCTTGAGCTATGGCTGGTGGAGATGAT 439
Db 279 TAGAGTCAAGCAGAAATCTGGCTTGGAGCTTGCAGCTATGGATGGTGGAGAACAT 338
Qy 440 TCGTGGTCACTCTAGAGTATAGCCCAACCCCAAGTGTGGGAAAATGGGTGGGTGCC 499
Db 339 TCTGTGTCATCCCTCGATTTCTCAACCCCGAGGTGGAGATGGCAAGGTGCC 398
Qy 500 TGATTTGAAGGTTCAGTGAGCCGACAGTTTGCAGCCTATTTGTACAACTCATCTGATA 559
Db 399 TGAATTTGAATGCTCCCTCCAGCCCAAAAGTTCAAGCCCTATTTGCCAACATCATCCGACA 458
Qy 560 CTTGAGCTAACTCGTGCATTCAGAAATATACCAACCAAGATCCCATATTTCAACATC 619
Db 459 CTTGAGTAACTCGTGCATTCAGAAATCGTTACCAATTTTACCCCGTGTGGACACTC 518
Qy 620 AAATGCAACACAAACAGAAATTTATTTGTCAGTGACAGTACCTACTCGGTGGCATCC 679
Db 519 A-----AACACCCGCAACAGATTTCTGTGACAGAGCGCCTACTTGGCTTCATCCC 572
Qy 680 CTTACTTACATACCTGCGCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTC 739
Db 573 CTGACTCCACAAACCTG---TTTCTGCGCACCCCGGCTCCACCTTTGACCTCCATGG 629
Qy 740 CACGAGAGAAAAATTCATTTGTGTCACAGAGTTTATGCGAACTAGACCACTGCTA 799
Db 630 CACGAGAGAAAAATTTGTATCAGGAAGTTTATACAGAACTTATCACCATGCTA 689
Qy 800 CAGAACTGCAACCAATTTGTTGAAAATTAAGCAGCATTTCAAGATGAAGCTGCTGGTTG 859
Db 690 CAGAAACAGAGCAATTTGTCAGTGGAGCAGCATTTCAAGAACAGAGCAGCTGGTTG 749
Qy 860 GAGTGTCCCAACGCTGTGCTAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 919
Db 750 GAGTGTCCCAACGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 809
Qy 920 TTGATTTGCTATGTCAGAAAGTATGTGAGGCTTCCCTCTCTCTCTCTCTCTCTCTCT 979
Db 810 TGGCTGTGCTATGTCAGAAAGTATGTGAGGCTTCCCTCTCTCTCTCTCTCTCTCTCT 869
Qy 980 AGAAGAAATCATCGAAACCAAGTATGTAAGGAGAGAGGCAATGATAGCAACCTA 1039
Db 870 AGAAGAAATCATCGAAACCAAGTATGTAAGGAGAGAGGCTGATGACGTCAACGCTA 929
Qy 1040 ATGAGAAATCAAGAAACCTGATATAAACCCAGAGAGTCCAGAGTCCAGCAAACTA 1099
Db 930 ATGAGAAATCAAGAAACCTATTAATAACCCAGAGAGGCAAGAGTCCACCAAACTA 989
Qy 1100 CCGTGGCATGCTGGAAGCTGAAGTTTAGATGACAGAAATGAGGAGACACACTGAGG 1159
Db 990 CGTGGCATGCTGGAAGCTGAAGTTTAGATGCAAGAGAGTGGAGAGGTCACACAGG 1049
Qy 1160 CTGGTTCTTTC 1171
Db 1050 CAAGTTTCATGC 1061

RESULT 9

US-08-892-880-11/c
; Sequence 11, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HERewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-892-880-11

Query Match 14.1%; Score 334; DB 2; Length 339;
Best Local Similarity 98.5%; Pred. No. 1.1e-85;
Matches 334; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1466 CCTCTCGCTGTCTGAGGCTAGGTGGCTTGAAGCCCAAGAGTCACTGAGACCAAGCTT 1525
Db 339 CCTCTCGCTGTCTGAGGCTAGGTGGCTTGAAGCCCAAGAGTCACTGAGACCAAGCTT 280
Qy 1526 TCTCTACTGATTCGGCAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCC 1585
Db 279 NCTCTACTGATTCGGCAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCC 220
Qy 1586 ACCTGACATCTCTTCTGAGCCCGGTAAAGCAAAAGATGGCAGAAAGTTTACCCCT 1645
Db 219 ACCTGACATCTCTTCTGAGCCCGGTAAAGCAAAAGATGGCAGAAAGTTTACCCCT 160
Qy 1646 GAAAGCCATCGAGATTCCTATACTTGAACCTTGAACCTTAATCTCTGTAAGCTTAAATAAGAAA 1705
Db 159 GAAAGCCATCGAGATTCCTATACTTGAACCTTGAACCTTAATCTCTGTAAGCTTAAATAAGAAA 100
Qy 1706 TAGAACAAGCTGAGGATACGACAGTACACTGTTCAGCAGGAGTGTAAACACAGACAGGG 1765
Db 99 TAGAACAAGCTGAGGATACGACAGTACACTGTTCAGCAGGAGTGTAAACACAGACAGGG 40
Qy 1766 TCAAGTGTCTTCTCTCAACACATTCAGTTGGATCACT 1804
Db 39 TCAAGTGTCTTCTCTCAACACATTCAGTTGGATCACT 1

RESULT 10

US-08-892-880-12
; Sequence 12, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
;; CITY: WASHINGTON
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/892,880
;; FILING DATE: HEREWITH
;; CLASSIFICATION: 435
;; PRIOR APPLICATION NUMBER: 60/021,762
;; FILING DATE: 15-JUL-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STEFFE, ERIC K
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.0490001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 492 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-08-892-880-12

Query Match 12.5%; Score 296.8; DB 2; Length 492;
Best Local Similarity 98.3%; Pred. No. 6.4e-75;
Matches 298; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 75 CATCGGACTAGTATTAGCATCTCCCTCATATCAACAGTGGCCATCTGAGGTGTTT 134
Db 14 CATCGGACTAGTATTAGCATCTCCCTCATATCAACAGTGGCCATCTGAGGTGTTT 73
QY 135 CCTGGCTCTGAAGGGTAGGACGATGGCCAGTGGCTTCAGCTGGTGTGCTTCTCAC 194
Db 74 CCTGGCTCTGAAGGGTAGGACGATGGCCAGTGGCTTCAGCTGGTGTGCTTCTCAC 133
QY 195 TTCCATCTGGACACAGAGGCTCTCGTCCAAGGCTCTTTGCGTGCAAGAGCTTTCCAT 254
Db 134 TTCCATCTGGACACAGAGGCTCTCGTCCAAGGCTCTTTGCGTGCAAGAGCTTTCCAT 193
QY 255 CCAGGTGTGATGAGAAATTATGGGATCACCCCTTGAGCAAAAAGCGACAGGCT 314
Db 194 CCAGGTGTGATGAGAAATTATGGGATCACCCCTTGAGCAAAAAGCGACAGGCT 253
QY 315 GAATTTACAGAGCTAAGAGCCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGA 374
Db 254 GAATTTACAGAGCTAAGAGCCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGA 313
QY 375 CCA 377
Db 314 CCA 316

RESULT 11
US-09-389-681-324/c
; Sequence 324, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun

;; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
;; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;; FILE REFERENCE: 210121.470C3
;; CURRENT APPLICATION NUMBER: US/09/389,681A
;; CURRENT FILING DATE: 1999-09-02
;; NUMBER OF SEQ ID NOS: 463
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 324
;; LENGTH: 241
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-389-681-324

Query Match 10.1%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1495 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTTACTGATTCGCGAGCTCAGACCCCTT 1554
Db 241 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTTACTGATTCGCGAGCTCAGACCCCTT 182
QY 1555 TCTTCAGCTCTGAAAGAGAAACACGATATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 1614
Db 181 TCTTCAGCTCTGAAAGAGAAACACGATATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 122
QY 1615 AGCAAAAGAATGCGAGAAAGTTTAGCCCTGAAAGCCATGAGATTTCTCATAACTTGAG 1674
Db 121 AGCAAAAGAATGCGAGAAAGTTTAGCCCTGAAAGCCATGAGATTTCTCATAACTTGAG 62
QY 1675 ACTAATCTCTGTAAGCTTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTAC 1733
Db 61 ACTAATCTCTGTAAGCTTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTAC 3

RESULT 12.

US-09-620-405B-324/c
; Sequence 324, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-324

Query Match 10.1%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1495 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTTACTGATTCGCGAGCTCAGACCCCTT 1554
Db 241 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTTACTGATTCGCGAGCTCAGACCCCTT 182
QY 1555 TCTTCAGCTCTGAAAGAGAAACACGATATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 1614
Db 181 TCTTCAGCTCTGAAAGAGAAACACGATATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 122
QY 1615 AGCAAAAGAATGCGAGAAAGTTTAGCCCTGAAAGCCATGAGATTTCTCATAACTTGAG 1674
Db 121 AGCAAAAGAATGCGAGAAAGTTTAGCCCTGAAAGCCATGAGATTTCTCATAACTTGAG 62

QY 1675 ACCTAATCTCTGTAAGCTAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTAC 1733
|
Db 61 ACCTAATCTCTGTAAGCTAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTAC 3

RESULT 13
US-09-433-826B-324/c
; Sequence 324, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-324

Query Match 10.1%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1495 GAAAGCCAAGGAGTCACCTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCCCTT 1554
|
Db 241 GAAAGCCAAGGAGTCACCTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCCCTT 182

QY 1555 TCCTTCAGCTCTGAAAGAGAAACACGTATCCACCTGCATGTCCTTCTGAGCCCGGTAAG 1614
|
Db 181 TCCTTCAGCTCTGAAAGAGAAACACGTATCCACCTGCATGTCCTTCTGAGCCCGGTAAG 122

QY 1615 AGCAAAAGATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTTGAG 1674
|
Db 121 AGCAAAAGATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTTGAG 62

QY 1675 ACCTAATCTCTGTAAGCTAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTAC 1733
|
Db 61 ACCTAATCTCTGTAAGCTAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTAC 3

RESULT 14
US-09-604-287A-324/c
; Sequence 324, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-324

Query Match 10.1%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1495 GAAAGCCAAGGAGTCACCTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCCCTT 1554
|
Db 241 GAAAGCCAAGGAGTCACCTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCCCTT 182

QY 1555 TCCTTCAGCTCTGAAAGAGAAACACGTATCCACCTGCATGTCCTTCTGAGCCCGGTAAG 1614
|
Db 181 TCCTTCAGCTCTGAAAGAGAAACACGTATCCACCTGCATGTCCTTCTGAGCCCGGTAAG 122

QY 1615 AGCAAAAGATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTTGAG 1674
|
Db 121 AGCAAAAGATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTTGAG 62

QY 1675 ACCTAATCTCTGTAAGCTAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTAC 1733
|
Db 61 ACCTAATCTCTGTAAGCTAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTAC 3

RESULT 15
US-09-834-759-324/c
; Sequence 324, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-324

Query Match 10.1%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1495 GAAAGCCAAGGAGTCACCTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCCCTT 1554
|
Db 241 GAAAGCCAAGGAGTCACCTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCCCTT 182

QY 1555 TCCTTCAGCTCTGAAAGAGAAACACGTATCCACCTGCATGTCCTTCTGAGCCCGGTAAG 1614
|
Db 181 TCCTTCAGCTCTGAAAGAGAAACACGTATCCACCTGCATGTCCTTCTGAGCCCGGTAAG 122

QY 1615 AGCAAAAGATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTTGAG 1674
|
Db 121 AGCAAAAGATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTTGAG 62

QY 1675 ACCTAATCTCTGTAAGCTAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTAC 1733
|
Db 61 ACCTAATCTCTGTAAGCTAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTAC 3

Search completed: August 16, 2004, 17:08:30
Job time : 176 secs

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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 08:16:11 ; Search time 9272 Seconds
(without alignments)
11088.188 Million cell updates/sec

Title: US-10-063-670-5
Perfect score: 2372
Sequence: 1 agcagggaatccggtgctc.....ttaagcatttagaaaactt 2372

Scoring table: IDENTIFY NUC
Gapop 10_0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues 6940544

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_pl.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_ba.*
- 15: em_fun.*
- 16: em_in.*
- 17: em_hum.*
- 18: em_mu.*
- 19: em_or.*
- 20: em_ov.*
- 21: em_ph.*
- 22: em_pl.*
- 23: em_ro.*
- 24: em_sts.*
- 25: em_un.*
- 26: em_vi.*
- 27: em_htg_hum.*
- 28: em_htg_inv.*
- 29: em_htg_other.*
- 30: em_htg_mus.*
- 31: em_htg_pln.*
- 32: em_htg_rod.*
- 33: em_htg_man.*
- 34: em_htg_vrt.*
- 35: em_sy.*
- 36: em_hgo_hum.*
- 37: em_hgo_mus.*
- 38: em_hgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2372	100.0	2372	6	AR410761	AR410761 Sequence
2	2372	100.0	2372	6	AX092274	AX092274 Sequence
3	2372	100.0	2372	6	AX454446	AX454446 Sequence
4	2372	100.0	2372	6	AX490324	AX490324 Sequence
5	2372	100.0	2372	6	AX697609	AX697609 Sequence
6	2372	100.0	2372	6	BD075532	BD075532 Secretary
7	2372	100.0	2372	6	BD172392	BD172392 Secretary
8	2372	100.0	2372	6	BD172711	BD172711 Secretary
9	2372	100.0	2372	6	BD173030	BD173030 Secretary
10	2372	100.0	2372	6	BD173349	BD173349 Secretary
11	2372	100.0	2372	6	BD175383	BD175383 Secretary
12	2372	100.0	2372	9	AY358925	AY358925 Homo sapi
13	2282.2	96.2	2313	9	AF118108	AF118108 Homo sapi
14	2245.4	94.7	2282	9	BC026231	BC026231 Homo sapi
15	1994	84.1	2029	6	AR204700	AR204700 Sequence
16	1994	84.1	2029	6	BD222718	BD222718 Human sig
17	1712.4	72.2	1755	6	AX136227	AX136227 Sequence
18	1712.4	72.2	1755	6	BD123566	BD123566 Secretary
19	1712.4	72.2	1755	9	AK075443	AK075443 Homo sapi
20	1437.2	60.6	165898	9	AC009532	AC009532 Homo sapi
21	1191.4	50.2	1285	9	AF127670	AF127670 Homo sapi
22	927.2	39.1	1613	4	AY372937	AY372937 Bos tauru
23	631.8	26.6	716	6	AX136529	AX136529 Sequence
24	631.8	26.6	716	6	BD123769	BD123769 Secretary
25	631	26.6	2027	10	BC038653	BC038653 Mus muscu
26	631	26.6	2027	10	BC038892	BC038892 Mus muscu
27	616.4	26.0	1516	10	MM0311501	AJ311501 Mus muscu
28	500.2	21.1	516	6	AX331191	AX331191 Sequence
29	500.2	21.1	516	6	AX331600	AX331600 Sequence
30	500.2	21.1	516	6	AX332298	AX332298 Sequence
31	500.2	21.1	516	6	AX333352	AX333352 Sequence
32	500.2	21.1	516	6	AX333777	AX333777 Sequence
33	500.2	21.1	516	6	AX407467	AX407467 Sequence
34	485.8	20.5	506	6	AX156239	AX156239 Sequence
35	458.8	19.3	591	6	AX136672	AX136672 Secretary
36	458.8	19.3	591	6	BD123912	BD123912 Secretary
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38	386.2	16.3	603	4	AY304537	AY304537 Sus scrof
39	343	14.5	363	6	BD077623	BD077623 5' EST of
40	331.8	14.0	373	6	BD073800	BD073800 5' EST of
41	246.4	10.4	250	11	GI4689	GI4689 SHGC-13369
42	239	10.1	241	6	AR280816	AR280816 Sequence
43	239	10.1	241	6	AR283312	AR283312 Sequence
44	239	10.1	241	6	AR344080	AR344080 Sequence
45	239	10.1	241	6	AR351281	AR351281 Sequence

ALIGNMENTS

RESULT 1	AR410761	Sequence 200 from patent US 6635468.	2372 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	AR410761	Sequence 200 from patent US 6635468.				
DEFINITION	AR410761	Sequence 200 from patent US 6635468.				
ACCESSION	AR410761.1	GI:40162261				
VERSION	AR410761.1	GI:40162261				
KEYWORDS		Unknown.				
SOURCE		Unknown.				
ORGANISM		Unclassified.				
REFERENCE	1 (bases 1 to 2372)					
AUTHORS	Ashkenazi, A., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Grimaldi, J.C., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,					

Pred. No. is the number of results predicted by chance to have a

Stewart, T.A., Tunas, D., Williams, P.M. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL Patent: US 6635468-A 200 21-OCT-2003;
FEATURES Location/Qualifiers

source 1..2372
/organism="unknown"

ORIGIN /mol_type="genomic DNA"

Query Match	100.0%;	Score 2372;	DB 6;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches 0;	Gaps 0;
Matches 2372;	Conservative 0;	Indels 0;		
QY	1	AGCAGGAAATCCCGATGCTCTCGGTTATGAAGTGGAGCAGTGGTGGAGCTCAACATA	60	
DB	1	AGCAGGAAATCCCGATGCTCTCGGTTATGAAGTGGAGCAGTGGTGGAGCTCAACATA	60	
QY	61	GTTCCAGAACTCTCCATCCGAGTCTGAGTATGAGATCTGGCTCTCATCACCAAGTGGC	120	
DB	61	GTTCCAGAACTCTCCATCCGAGTCTGAGTATGAGATCTGGCTCTCATCACCAAGTGGC	120	
QY	121	CATCTGAGTGTTCCTCGGCTCTCAAGGGTAGGCAAGTGGTGGTGGTGGTGGTGGTGG	180	
DB	121	CATCTGAGTGTTCCTCGGCTCTCAAGGGTAGGCAAGTGGTGGTGGTGGTGGTGGTGG	180	
QY	181	GTTGTGCTTCTCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	240	
DB	181	GTTGTGCTTCTCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	240	
QY	241	GAAGAGCTTTCATCCAGGCTGATGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	300	
DB	241	GAAGAGCTTTCATCCAGGCTGATGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	300	
QY	301	GCAGAACAGCAGTGAATTTACAGAGCTGAAGAGGCTGAGGCTGAGGCTGAGGCTGAG	360	
DB	301	GCAGAACAGCAGTGAATTTACAGAGCTGAAGAGGCTGAGGCTGAGGCTGAGGCTGAG	360	
QY	361	TTGCGCGGACAGGACCAAGTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA	420	
DB	361	TTGCGCGGACAGGACCAAGTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA	420	
QY	421	GGCTGGCTTGGAGTGAATTCGTTGAGGCTGAGTGAATTCGTTGAGGCTGAGTGAAT	480	
DB	421	GGCTGGCTTGGAGTGAATTCGTTGAGGCTGAGTGAATTCGTTGAGGCTGAGTGAAT	480	
QY	481	AAAAATGGGCTGGGCTGCTGATTTGAAGCTTCAAGTGGTGGTGGTGGTGGTGGTGG	540	
DB	481	AAAAATGGGCTGGGCTGCTGATTTGAAGCTTCAAGTGGTGGTGGTGGTGGTGGTGG	540	
QY	541	TGTTACAACTCATCTGATCTGGACTTAACCTGTCGATTCGAGTGAATTCACCAACAA	600	
DB	541	TGTTACAACTCATCTGATCTGGACTTAACCTGTCGATTCGAGTGAATTCACCAACAA	600	
QY	601	GATCCCAATATCAACCTCAACTGCAACCAACCAACCAACCAACCAACCAACCAACCA	660	
DB	601	GATCCCAATATCAACCTCAACTGCAACCAACCAACCAACCAACCAACCAACCAACCA	660	
QY	661	ACCTACTCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	720	
DB	661	ACCTACTCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	720	
QY	721	CCAGCTTCCATCTTATTCACCGAGAAATATGATTTGTTGTTGTTGTTGTTGTTGTTG	780	
DB	721	CCAGCTTCCATCTTATTCACCGAGAAATATGATTTGTTGTTGTTGTTGTTGTTGTTG	780	
QY	781	GAACTAGACCACTGCTACAGAACTGACCAATTTGTTGAAATTAAGCAGATTCAG	840	
DB	781	GAACTAGACCACTGCTACAGAACTGACCAATTTGTTGAAATTAAGCAGATTCAG	840	
QY	841	AATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGGTCTCTCTCTTC	900	
DB	841	AATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGGTCTCTCTCTTC	900	

QY	901	TTTGTGCTGCTGAGCTGGTCTTGGATTTTGGTATGTCAAAGCTATCTGAAGCTTCCCT	960	
DB	901	TTTGTGCTGCTGAGCTGGTCTTGGATTTTGGTATGTCAAAGCTATCTGAAGCTTCCCT	960	
QY	961	TTTCAAAAACAAGATCAGCAGAGGAAATGATCGAAAACCAAGTATGTAAGGAGGAGAAG	1020	
DB	961	TTTCAAAAACAAGATCAGCAGAGGAAATGATCGAAAACCAAGTATGTAAGGAGGAGAAG	1020	
QY	1021	GCATATGATGCAACCTTAATGAGGAATCAAGAAAACCTGATAAAAACCCAGAGAGTCC	1080	
DB	1021	GCATATGATGCAACCTTAATGAGGAATCAAGAAAACCTGATAAAAACCCAGAGAGTCC	1080	
QY	1081	AAGAGTCCAAAGCAAACTACCGTGGATGCGTGGAGCTGGAAGTGAAGTTTACATGAGCAGAA	1140	
DB	1081	AAGAGTCCAAAGCAAACTACCGTGGATGCGTGGAGCTGGAAGTGAAGTTTACATGAGCAGAA	1140	
QY	1141	TAAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCTTACCTGCCCCCAGCTGGGAA	1200	
DB	1141	TAAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCTTACCTGCCCCCAGCTGGGAA	1200	
QY	1201	ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCCTTAACCTGGAATCAGC	1260	
DB	1201	ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCCTTAACCTGGAATCAGC	1260	
QY	1261	TCAGAGCTGCGCATTTGGACTATGGAGTGCAACCAAGAGAAATGCCCTTCTTATTTTAAAC	1320	
DB	1261	TCAGAGCTGCGCATTTGGACTATGGAGTGCAACCAAGAGAAATGCCCTTCTTATTTTAAAC	1320	
QY	1321	CCTGTGGAATCTTATCTCTTACCTCAAAAGCTTCCACGGCTTTCTAGCTGGCTAT	1380	
DB	1321	CCTGTGGAATCTTATCTCTTACCTCAAAAGCTTCCACGGCTTTCTAGCTGGCTAT	1380	
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VERSION AX092274.1 GI:13444451
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Eaton, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: WO 0116318-A 5 08-MAR-2001;
Genentech, Inc. (US)
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ORIGIN
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Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX454446 2372 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 31 from Patent WO0208284.
ACCESSION AX454446
VERSION AX454446.1 GI:21713847
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Strehn, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0208284-A 31 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
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DEFINITION Sequence 31 from Patent WO0200690.
ACCESSION AX490924
VERSION AX490924.1 GI:22323799
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
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Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0200690-A 31 03-JAN-2002;
Genentech, Inc. (US)

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Db	61	GTTCAGAACTCTCCATCCGAGTATGTTATTGAGCATCTGCTCTCATATCACAGTGGC	120		
QY	121	CATCTGAGTGTTCCTGGTCTGAAGGGTAGGCAGATGGCCAGGTGCTTCAGCCTG	180		
Db	121	CATCTGAGTGTTCCTGGTCTGAAGGGTAGGCAGATGGCCAGGTGCTTCAGCCTG	180		
QY	181	GTGTCCTTCTCACTTCCATCTGACACAGAGGCTCTGGTCCAAAGGCTCTTTGGTGCA	240		
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QY	241	GAAGAGCTTTCATCCAGTGTCTATGAGAAATATGGGATCACCTGTGAGCAAAAG	300		
Db	241	GAAGAGCTTTCATCCAGTGTCTATGAGAAATATGGGATCACCTGTGAGCAAAAG	300		
QY	301	CGCAACACAGAGCTGAATTTACAGAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGT	360		
Db	301	CGCAACACAGAGCTGAATTTACAGAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGT	360		
QY	361	TTGCCGCGAGGACCAAGTTGAACAGCCTTGAAGCTAGCTTTGAACCTTGAGCTAT	420		
Db	361	TTGCCGCGAGGACCAAGTTGAACAGCCTTGAAGCTAGCTTTGAACCTTGAGCTAT	420		
QY	421	GGCTGGGTGGAGATGGATTCGTGCTCATCTAGGATTAGCCCAACCCCAAGTGTGGG	480		
Db	421	GGCTGGGTGGAGATGGATTCGTGCTCATCTAGGATTAGCCCAACCCCAAGTGTGGG	480		
QY	481	AAAAATGGGTGGGTGCTGATTTGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540		
Db	481	AAAAATGGGTGGGTGCTGATTTGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540		
QY	541	TGTTAACACTCATCTGATCTGACTAACTCGTGCATTCCAGAAATTTATCACCAACAA	600		
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Db	661	ACCTACTGGGTGGATCCCTTACTCTAACAATACTGCCCCCTACTACTCTCTCTCTCT	720		
QY	721	CCAGCTTCCACTTCTATTCCACGAGAAATAATGATTTGTGTCACAGAGTTTATTATG	780		
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QY	901	TTTGGTGTGCTGAGTGTGTTGGATTTTGTCTATGTCATAAAGGATGTGAGGCTTCCCT	960		

Db	901	TTTGGTGTGCTGAGCTGGTCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAAGCTTCCCT	960
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QY	1021	GCCATGATAGCAACCTTAATGAGGAATCAAGAAATCTGATAAAACCCAGAGAGTCC	1080
Db	1021	GCCATGATAGCAACCTTAATGAGGAATCAAGAAATCTGATAAAACCCAGAGAGTCC	1080
QY	1081	AAGAGTCAAGCAAAACTACCGTGGATGCTGGAAGCTGAAGTTAGTAGAGACAGAAA	1140
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QY	1321	CCTGCTGGATCTTATCTCTCTACCTCAAGCTTCCACGGCTTCTAGCTGGCTAT	1380
Db	1321	CCTGCTGGATCTTATCTCTCTACCTCAAGCTTCCACGGCTTCTAGCTGGCTAT	1380
QY	1381	GTCTCTAATAATATCCCACTGGGAGAAAGGATTTGCAAGTGCAAGGACCTAAACATC	1440
Db	1381	GTCTCTAATAATATCCCACTGGGAGAAAGGATTTGCAAGTGCAAGGACCTAAACATC	1440
QY	1441	TCATCAGTATCCAGTGTAAGAAAGGCTCTCGGCTGTCTGAGGCTAGTGCGTTGAAAGC	1500
Db	1441	TCATCAGTATCCAGTGTAAGAAAGGCTCTCGGCTGTCTGAGGCTAGTGCGTTGAAAGC	1500
QY	1501	CAAGAGTCACTGAGACCAAGGCTTCTCTACTGATCCGAGCTCAGACCTTCTTCA	1560
Db	1501	CAAGAGTCACTGAGACCAAGGCTTCTCTACTGATCCGAGCTCAGACCTTCTTCA	1560
QY	1561	GCTCTGAAGAGAAACAGTATCCCACTGATCTCTCTGAGCCCGGTAAAGAGCAAA	1620
Db	1561	GCTCTGAAGAGAAACAGTATCCCACTGATCTCTCTGAGCCCGGTAAAGAGCAAA	1620
QY	1621	AGATGCGAGAAAGTTTGGCCCTGAAAGCCATGGAGATTTCTATTAATTTGAGACCTAA	1680
Db	1621	AGATGCGAGAAAGTTTGGCCCTGAAAGCCATGGAGATTTCTATTAATTTGAGACCTAA	1680
QY	1681	TCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA	1740
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1561	DB	GCTCTGAAAGAGAAACACGTATCCCACTGACATGTCTTCTGAGCCCGGTAAAGCAAA	1620
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1621	DB	AGAAATGCGCAAGAAAGTTTACGCCCTGAAAGCCATGGAGATCTCATAACTTGGACCTAA	1680
1681	QY	TCTCTGTAAAGCTTAAAAATAAGAAATAGAAACAAGGCTTGAGGATACGACAGTCACTGTCA	1740
1681	DB	TCTCTGTAAAGCTTAAAAATAAGAAATAGAAACAAGGCTTGAGGATACGACAGTCACTGTCA	1740
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2161	DB	GACTAATCTTATTCAATTTTCTTAATATGCAACCACTATAACCTTAAATTTATTTAAAC	2220
2221	QY	ATACCTTAAGAGTACATTTGTTACTCTATATATCAAGACATTTTAAAGTGCCTATTAA	2280
2221	DB	ATACCTTAAGAGTACATTTGTTACTCTATATATCAAGACATTTTAAAGTGCCTATTAA	2280
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DEFINITION	BD075532				
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VERSION	GI:22621135				
KEYWORDS	JP 2001516580-A/165.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.				
AUTHORS	(bases 1 to 2372)				
TITLE	Secretory and transmembrane polypeptide and nucleic acid encoding the same				
JOURNAL	Patent: JP 2001516580-A 165 02-OCT-2001;				
	GENENTECH INC				
COMMENT	OS Homo sapiens (human)				
	PN JP 2001516580-A/165				
	PD 02-OCT-2001				
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	25-NOV-1997 US 60/066840				
PI	WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI JEAN CHEN,				
PI	JEAN YUAN				
PC	C12N15/09, C07K14/47, C07K14/705, C07K16/18, C07K16/28, C07K19/00,				
PC	C12N1/19				
PC	C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12Q1/02, C12P21/08, PC C12R1.91),				
PC	C12N15/00, C12N5/00				
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FT	Location/Qualifiers				
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ORIGIN					
Query Match	100.0%; Score 2372; DB 6; Length 2372;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches 2372; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
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Db 1 AGCAGGAAATCCGATGCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
Qy 61 GTTCAGAACTCTCCATCGGACTAGTTATTGAGCAATCTGCTCTCATATACACAGTGGC 120
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Qy 121 CATCTGAGGTGTTCCCTGGCTCTCAAGGGTAGGCACGATGGCCAGGTGCTTACGCTG 180
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BD172392 2372 bp DNA linear PAT 18-FEB-2003
 DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding
 the same.
 BD172392
 VERSION BD172392.1 GI:28413692
 KEYWORDS JP 2002223786-A/165.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2372)
 AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
 Yuan,J.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: JP 2002223786-A 165 13-AUG-2002;
 GENENTECH INC
 COMMENT OS Homo sapiens (human)
 PN JP 2002223786-A/165
 PD 13-AUG-2002
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LOCUS

DEFINITION

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING

THE SAME.

ACCESSION

BD173349

VERSION

GI:28414660

KEYWORDS

UP 2002238588-A/165.

SOURCE

Homo sapiens (human).

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2372)

AUTHORS

Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and

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TITLE

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Patent: JP 2002238588-A 165 27-AUG-2002;
GENENTECH INC
OS Homo sapiens (human)
PN JP 2002238588-A/165
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DEFINITION Secretary and transmembrane polypeptide and nucleic acid encoding the same.

ACCESSION BD175383

VERSION BD175383.1 GI:29121079

KEYWORDS JP 2002253280-A/165.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2372)

Wood, M.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.

Secretary and transmembrane polypeptide and nucleic acid encoding the same

PATENT: JP 2002253280-A 165 10-SEP-2002;

GENENTECH INC

OS Homo sapiens (human)

PN JP 2002253280-A/165

PD 10-SEP-2002

PF 18-DEC-2001 JP 2001385319

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17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR

17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR

17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR

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WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09, A61K45/00, A61P1/00, A61P13/12, A61P17/00, A61P17/06, PC A61P25/00,

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 VERSION
 KEYWORDS FLI CDNA
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

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 FLI CDNA
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 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
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REFERENCE
 1 (bases 1 to 2372)
 Clark.H.F., Gurney A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
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 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
 Goddard,A., Wood,W.I. and Godowski,P.
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment
 Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL
 PUBMED 12975309
 REFERENCE 2 (bases 1 to 2372)
 Clark.H.F.
 Direct Submission
 TITLE Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA
 JOURNAL Location/Qualifiers

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ORIGIN

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AF118108
VERSION
AF118108.1 GI:5359672
KEYWORDS
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 (bases 1 to 2313)
Banerji,S., Ni,J., Wang,S.X., Clasper,S., Su,J., Tammi,R., Jones,M.
and Jackson,D.G.
LYVE-1, a new homologue of the CD44 glycoprotein, is a
lymph-specific receptor for hyaluronan
J. Cell Biol. 144 (4), 789-801 (1999)
PUBMED
10037799
REFERENCE
2 (bases 1 to 2313)
Jackson,D.G., Banerji,S. and Ni,J.
Direct Submission
Submitted (06-JAN-1999) MRC Human Immunology Unit, Univ. of Oxford,
John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK
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VERSION	BC026231.1		
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TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
MEDLINE	22388257		
PUBMED	12477932		
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AUTHORS	Strausberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapps@mail.nih.gov Tissue Procurement: CLONTECH cDNA Library Preparation: CLONTECH Laboratories, Inc. DNA Sequencing by: The I.M.A.G.E. Consortium (ILNL) Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www.shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Drickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov			
Series: IRAL Plate: 37 Row: C Column: 20			
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729910.			
FEATURES	Location/Qualifiers		
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	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="MGC:22159 IMAGE:4712863"		
	/tissue type="Liver"		

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DB 264 GAAGAGCTTTCATCCAGGTGTCATGAGAAATATGAGGATCACCCCTGTGAGCAAAAAG 323
QY 301 GGAAACACAGCTGAATTTACAGAGCTAAGAGGCTGTAGGCTGTGGAGCTAAGT 360
DB 324 GGAAACACAGCTGAATTTACAGAGCTAAGAGGCTGTAGGCTGTGGAGCTAAGT 383
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DB 2004 TTCAACAAACATTTAAAAAAA 2025

Search completed: August 16, 2004, 15:24:08
Job time : 9282 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2004, 16:57:05 ; Search time 880 Seconds

(without alignments)
11450.825 Million cell updates/sec

Title: US-10-063-670-5

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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 800 summaries

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5: Geneseqn2001bs.*

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8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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93	1994	84.1	2029	3	AAZ98172 Human PRO
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95	1733	73.1	2967	3	AAZ59803 Human PRO
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97	1029	43.4	1680	9	ADD04999	Adcd04999 Human sec	170	53.6	2.3	700	4	AAH933026	Aah933026 Human inf
98	967.4	40.8	1127	7	ACA10111	Aca10111 Human NOV	c 171	53	2.2	6544	4	AA545340	Aas45340 Chemical
99	631.8	26.6	716	5	RAF94017	Raf94017 Primer sp	c 172	53	2.2	6544	6	ABL32646	Ab132646 Human imm
100	603.6	25.4	1896	6	AAI0132	Aai0132 Mouse lym	c 173	53	2.2	8101	6	ABL33979	Ab133979 Human imm
101	603.6	25.4	1896	6	ABL35066	Ab135066 Murine cD	c 174	53	2.2	8101	6	ABL33317	Ab133317 Human imm
102	526	22.2	586	6	ABT09892	Abt09892 Human bre	c 175	51.8	2.2	9832	6	ABL32656	Ab132656 Human imm
103	500.2	21.1	516	6	ABL65949	Ab165949 Lung can	c 176	51.6	2.2	16750	4	AA546314	Aas46314 Tumour su
104	500.2	21.1	516	6	ABL64470	Ab164470 Stomach c	c 177	51.6	2.2	16750	4	ABL32521	Ab132521 Human imm
105	500.2	21.1	516	6	ABL63363	Ab163363 Breast ca	c 178	51	2.2	20579	6	ABQ67074	Abq67074 Human ang
106	500.2	21.1	516	6	ABL63772	Ab163772 Breast ca	c 179	50.8	2.1	5407	6	ABL34090	Ab134090 Human imm
107	500.2	21.1	516	6	ABL65524	Ab165524 Lung can	c 180	50.6	2.1	392	7	ABX39643	Abx39643 Bovine ES
108	500.2	21.1	516	6	ABN93616	Abn93616 Gene #114	c 181	50.6	2.1	5504	6	ABL70350	Ab170350 Chemical
109	485.8	20.5	506	4	AAB55571	Aab55571 Human bre	c 182	50.6	2.1	5504	6	AA561309	Aas61309 Human gen
110	458.8	19.3	591	5	AAF94166	Aaf94166 Primer sp	c 183	50.4	2.1	8056	7	ABZ10100	Abz10100 Haematopo
111	450	19.0	451	2	AXA41156	Axa41156 Human sec	c 184	50.4	2.1	12237	6	ABL34358	Ab134358 Human imm
112	440	18.5	486	8	ACH22304	Ach22304 Human adu	c 185	50	2.1	50	2	AX52401	Aax52401 Probe use
113	419.4	17.7	472	8	ACH22239	Ach22239 Human adu	c 186	50	2.1	50	3	ADC78525	Adc78525 Human PRO
114	406	17.1	499	8	ACH30085	Ach30085 Human tes	c 187	50	2.1	50	4	AAF72559	Aaf72559 Human PRO
115	403	17.0	441	8	ACH17082	Ach17082 Human adu	c 188	50	2.1	50	7	ACA59064	Aca59064 Human PRO
116	397	16.7	411	8	ACH20895	Ach20895 Human adu	c 189	50	2.1	50	7	ACA58461	Aca58461 Probe #38
117	387.6	16.3	820	10	ADE71448	Ade71448 Dog cDNA	c 190	50	2.1	50	7	ACA60168	Aca60168 Human sec
118	343	14.5	363	2	AXA41003	Axa41003 Human sec	c 191	50	2.1	50	7	ACD07568	Acd07568 Novel hum
119	331.8	14.0	373	2	AXA51631	Axa51631 Human sec	c 192	50	2.1	50	7	ABX71616	Abx71616 Human sec
120	328.6	13.9	559	10	ADE71446	Ade71446 Rat cDNA	c 193	50	2.1	50	7	ACH06948	Ach06948 Human sec
121	239	10.1	241	4	AAF17836	Aaf17836 Human bre	c 194	50	2.1	50	7	ABX96185	Abx96185 Human sec
122	239	10.1	241	4	AA547266	Aas47266 Human bre	c 195	50	2.1	50	7	ACA05506	Aca05506 Human sec
123	239	10.1	241	6	ABS63867	Abs63867 Human bre	c 196	50	2.1	50	7	ACD20173	Acd20173 Human sec
124	239	10.1	241	7	ABT33079	Abt33079 Human tum	c 197	50	2.1	50	7	ACA54976	Aca54976 Novel sec
125	239	10.1	241	10	ADE44276	Ade44276 Human cDN	c 198	50	2.1	50	8	ACD19811	Acd19811 Human sec
126	238	10.0	308	6	ABL63797	Ab163797 Breast ca	c 199	50	2.1	50	8	ADB29410	Adb29410 Human sec
127	238	10.0	308	6	ABL63384	Ab163384 Breast ca	c 200	50	2.1	50	8	ADA18266	Ada18266 Human sec
128	238	10.0	308	6	ABL63798	Ab163798 Breast ca	c 201	50	2.1	50	8	ADC66958	Acd66958 Human sec
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130	237	10.0	241	4	AAF17835	Aaf17835 Human bre	c 203	50	2.1	50	8	ADA16241	Ada16241 Human sec
131	237	10.0	241	4	AA547265	Aas47265 Human bre	c 204	50	2.1	50	8	ADA42386	Ada42386 Human sec
132	237	10.0	241	6	ABS63866	Abs63866 Human bre	c 205	50	2.1	50	8	ACD23297	Acd23297 Human PRO
133	237	10.0	241	7	ABT33078	Abt33078 Human tum	c 206	50	2.1	50	8	ADA16665	Ada16665 Human sec
134	236	10.0	241	10	ADE44275	Ade44275 Human cDN	c 207	50	2.1	50	8	ADA13094	Ada13094 Human sec
135	226.2	9.5	239	6	ABL65603	Ab165603 Lung can	c 208	50	2.1	50	8	ADA11962	Ada11962 Human sec
136	226.2	9.5	239	6	ABL63605	Ab163605 Breast ca	c 209	50	2.1	50	8	ADA17309	Ada17309 Human sec
137	226.2	9.5	239	6	ABL66203	Ab166203 Lung can	c 210	50	2.1	50	8	ADA42812	Ada42812 Human sec
138	226.2	9.5	239	6	ABL64015	Ab164015 Breast ca	c 211	50	2.1	50	8	ADC23659	Acd23659 Human PRO
139	226.2	9.5	239	6	ABN94227	Abn94227 Gene #725	c 212	50	2.1	50	9	ADB77731	Adb77731 Human sec
140	212.2	8.9	279	10	ADE71447	Ade71447 Rat cDNA	c 213	50	2.1	50	9	ADC28513	Acd28513 Human sec
141	179.2	7.6	469	4	ARA54110	Ara54110 Human foe	c 214	50	2.1	50	9	ADC39713	Acd39713 Human sec
142	179.2	7.6	469	4	AAI33763	Aai33763 Probe #24	c 215	50	2.1	50	9	ADC40227	Acd40227 Human sec
143	179.2	7.6	469	4	ABA23859	Aba23859 Probe #23	c 216	50	2.1	50	9	ADC19051	Acd19051 Human sec
144	179.2	7.6	469	4	AAK27829	Aak27829 Human bon	c 217	50	2.1	50	9	ADC34351	Acd34351 Human sec
145	179.2	7.6	469	4	ABS27409	Abs27409 Human liv	c 218	50	2.1	50	9	ADC29406	Acd29406 Human sec
146	179.2	7.6	469	4	ABS02280	Abs02280 Human gen	c 219	50	2.1	50	9	ADC28937	Acd28937 Human sec
147	175	7.4	457	4	AAI33382	Aai33382 Probe #20	c 220	50	2.1	50	9	ADC40822	Acd40822 Human sec
148	175	7.4	457	4	ABS01959	Abs01959 Human gen	c 221	50	2.1	50	9	ADC19479	Acd19479 Human sec
149	129	5.4	141	4	ARA66678	Ara66678 Human foe	c 222	50	2.1	50	9	ADC33927	Acd33927 Human sec
150	129	5.4	141	4	AAI46891	Aai46891 Probe #15	c 223	50	2.1	50	9	ADC12997	Acd12997 Human sec
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153	129	5.4	141	6	ABS40414	Abs40414 Human liv	c 226	50	2.1	50	9	ADD04010	Add04010 Human sec
154	129	5.4	141	6	ABS14788	Abs14788 Human gen	c 227	50	2.1	50	9	ADD03586	Add03586 Human sec
155	106	4.5	106	4	AAI46523	Aai46523 Probe #15	c 228	50	2.1	50	9	ABE34838	Abe34838 Human sec
156	106	4.5	106	6	ABS14478	Abs14478 Human gen	c 229	50	2.1	50	9	ABE34838	Abe34838 Human sec
157	60	2.5	60	6	ABN38121	Abn38121 Human epl	c 230	50	2.1	50	10	ADE79283	Ade79283 Human sec
158	58.2	2.5	645	6	ABQ56694	Abq56694 Human col	c 231	50	2.1	50	10	ADE79707	Ade79707 Human sec
159	56.8	2.4	8056	7	ABZ10100	Abz10100 Haematopo	c 232	50	2.1	50	10	ADE73383	Ade73383 Human sec
160	56.6	2.4	2000	7	ADA71938	Ada71938 Rice gene	c 233	50	2.1	50	10	ADE73918	Ade73918 Human sec
161	56.6	2.4	6216	6	ABK39932	Abk39932 Human che	c 234	50	2.1	37515	6	ABQ66998	Abq66998 Human ang
162	56.6	2.4	6216	6	ABL70139	Ab170139 Chemical	c 235	49.6	2.1	47108	6	ABK31511	Abk31511 Signal tr
163	55.8	2.4	8056	7	ABZ10246	Abz10246 Haematopo	c 236	49.4	2.1	8305	6	AB133569	Ab133569 Human imm
164	55.4	2.3	339	7	ACC43051	Acc43051 Nucleotid	c 237	49.4	2.1	47841	6	ABQ80553	Abq80553 Human Can
165	55.2	2.3	8056	7	ABZ10246	Abz10246 Haematopo	c 238	49.4	2.1	73334	6	ABL34125	Ab134125 Human imm
166	55	2.3	83391	7	ABQ67093	Abq67093 Human ang	c 239	49.4	2.1	73334	6	ABL92319	Ab192319 Chemical
167	54.2	2.3	11922	3	AA70187	Aa70187 Plasmodi	c 240	49.2	2.1	7461	6	ABL33784	Ab133784 Human imm
168	54.2	2.3	15373	6	ABL32467	Ab132467 Human imm	c 241	49.2	2.1	21354	4	AB46815	Aas46815 Tumour su
169	53.8	2.3	11790	6	ABL32542	Ab132542 Human imm	c 242	49.2	2.1	302250	6	ABL67703	Ab167703 Oesophagu

C 243	49	2.1	5430	4	AAS46292	Aas46292 Tumour su	316	48.2	2.0	3476	10	AD564525	Ad564525 Human PRO
244	49	2.1	6106	4	AAS46429	Aas46429 Tumour su	317	48.2	2.0	3476	10	AD38860	Ad38860 Human PRO
245	49	2.1	6106	4	ABK40031	Abk40031 Human che	318	48.2	2.0	3476	10	AD51934	Ad51934 Human CDN
246	49	2.1	6106	6	ABL33472	Ab133472 Human imm	319	48.2	2.0	3476	10	ADD90965	AdD90965 Human CDN
247	49	2.1	15767	6	ABL33207	Ab133207 Human imm	320	48.2	2.0	3476	10	AD38744	Ad38744 Human PRO
248	49	2.1	15767	6	ABL34553	Ab134553 Human met	321	48.2	2.0	3476	10	AD37444	Ad37444 Human CDN
C 249	48.8	2.1	9810	6	ABL32426	Ab132426 Human imm	322	48.2	2.0	3476	10	AD506261	Ad506261 Human PRO
C 250	48.8	2.1	12025	6	ABL33299	Ab133299 Human imm	323	48.2	2.0	3476	10	AD90120	Ad90120 Human CDN
C 251	48.8	2.1	13202	6	ABL33485	Ab133485 Human imm	324	48.2	2.0	3476	10	AD38628	Ad38628 Human PRO
C 252	48.8	2.1	13722	6	ABL33530	Ab133530 Human imm	325	48.2	2.0	3476	10	AD39559	Ad39559 Human PRO
C 253	48.8	2.1	32392	6	ABL56203	Ab156203 AmEPV gen	326	48.2	2.0	3476	10	ADD89164	AdD89164 Human PRO
254	48.6	2.0	6154	6	ABL31200	Abk31200 Signal tr	327	48.2	2.0	3476	10	AD88931	Ad88931 Human PRO
255	48.6	2.0	6154	6	ABL70167	Ab170167 Chemicall	328	48.2	2.0	3476	10	AD19825	Ad19825 Human PRO
256	48.6	2.0	6154	6	AAS61112	Aas61112 Human gen	329	48.2	2.0	3476	10	AD77403	Ad77403 Human CDN
C 257	48.6	2.0	10749	2	AAS20257	Aax20257 Borrelia	330	48.2	2.0	3476	10	AD65279	Ad65279 Human PRO
C 258	48.6	2.0	11172	6	ABL34053	Ab134053 Human imm	331	48.2	2.0	3476	10	AD39327	Ad39327 Human PRO
259	48.6	2.0	17137	6	ABL32191	Ab132191 Human imm	332	48.2	2.0	3476	10	AD38512	Ad38512 Human CDN
C 260	48.4	2.0	6775	6	ABQ67160	Abq67160 Human ang	C 333	48.2	2.0	5430	4	AAS28917	Aas28917 Human imm
261	48.4	2.0	110000	6	ABA92787_3	Continuation (4 of	C 334	48.2	2.0	5430	9	ADB31758	Adb31758 Human nov
262	48.2	2.0	972	4	ABA06490_	Aba06490 Human CDN	C 335	48.2	2.0	6106	4	AAS46429	Aas46429 Tumour su
263	48.2	2.0	972	6	ABV83827	Abv83827 Human pol	C 336	48.2	2.0	6106	6	ABK40031	Abk40031 Human che
264	48.2	2.0	1587	2	AAV41923	Aav41923 Nucleotid	C 337	48.2	2.0	6106	6	ABL33472	Ab133472 Human imm
265	48.2	2.0	1720	2	AAV34136	Aav34136 Human sec	C 338	48	2.0	5362	6	ABK28414	Abk28414 DNA trans
266	48.2	2.0	1720	7	ACD08067	Acd08067 cDNA enco	339	47.8	2.0	47108	6	ABK31511	Abk31511 Signal tr
267	48.2	2.0	2013	4	AAF29460	Aaf29460 Human TAN	C 340	47.6	2.0	700	4	AHH93026	Aah93026 Human inf
268	48.2	2.0	2013	7	ACD66767	Acd66767 Secreted	C 341	47.6	2.0	9965	6	ABL33527	Ab133527 Human imm
269	48.2	2.0	2013	8	ADB90775	Adb90775 Human TAN	C 342	47.6	2.0	12578	4	AAS46660	Aas46660 Tumour su
270	48.2	2.0	2496	2	AAx20297	Aax20297 Borrelia	343	47.6	2.0	12781	4	AAS46385	Aas46385 Tumour su
271	48.2	2.0	2730	4	AAF29459	Aaf29459 Human TAN	344	47.6	2.0	12781	6	ABL92228	Ab192228 Chemicall
272	48.2	2.0	2730	7	ACD66766	Acd66766 Secreted	345	47.6	2.0	12781	9	AD854127	Ad854127 Pretreate
273	48.2	2.0	2730	8	ADB90774	Adb90774 Human CDN	346	47.6	2.0	12781	9	AD54255	Adb54255 Pretreate
274	48.2	2.0	2878	7	ADA48133	Ada48133 Human cho	347	47.6	2.0	32392	6	ABL56203	Ab156203 AmEPV gen
275	48.2	2.0	3476	4	AA31017	Aa31017 Human sec	C 348	47.4	2.0	40862	6	ABL34073	Ab134073 Human imm
276	48.2	2.0	3476	6	ABK69986	Abk69986 cDNA enco	C 349	47.2	2.0	883	4	AAS46694	Aas46694 Tumour su
277	48.2	2.0	3476	8	ADA01319	Ada01319 Human PRO	350	47.2	2.0	5413	4	AA456210	Aal15210 Human bre
278	48.2	2.0	3476	8	ADA43748	Ada43748 Human CDN	351	47.2	2.0	6074	6	ABK28374	Abk28374 DNA trans
279	48.2	2.0	3476	8	ADA43516	Ada43516 Human CDN	C 352	47.2	2.0	6174	4	AAS46433	Aas46433 Tumour su
280	48.2	2.0	3476	8	ADA01191	Ada01191 Human PRO	353	47.2	2.0	6191	6	ABL33216	Ab133216 Human imm
281	48.2	2.0	3476	8	ADA01075	Ada01075 Human CDN	354	47.2	2.0	6191	6	ABK31306	Abk31306 Signal tr
282	48.2	2.0	3476	8	ADA43632	Ada43632 Human CDN	355	47.2	2.0	6191	6	ABL70281	Ab170281 Chemicall
283	48.2	2.0	3476	8	ADA06894	Ada06894 Human PRO	356	47.2	2.0	6191	6	ABN80160	Abn80160 Human che
284	48.2	2.0	3476	8	ADA08382	Ada08382 Novel hum	C 357	47.2	2.0	7669	6	ABL32628	Ab132628 Human imm
285	48.2	2.0	3476	8	ADB99675	Adb99675 Human PRO	C 358	47.2	2.0	17137	6	ABL32191	Ab132191 Human imm
286	48.2	2.0	3476	8	ADB86958	Adb86958 Human PRO	C 359	47.2	2.0	17144	4	AAS46665	Aas46665 Tumour su
287	48.2	2.0	3476	8	ADB66113	Adb66113 Human CDN	C 360	47.2	2.0	19236	6	ABN80227	Abn80227 Human che
288	48.2	2.0	3476	9	ADB99791	Adb99791 Human PRO	C 361	47.2	2.0	110000	5	AA161373_0	Aa161373 Soybean 3
289	48.2	2.0	3476	9	ADB99446	ADB99446 Novel hum	C 362	47	2.0	4045	4	AAS46740	Aas46740 Tumour su
290	48.2	2.0	3476	9	ADB65997	Adb65997 Human CDN	C 363	47	2.0	5006	5	AD22381	Aad22381 Cotton ol
291	48.2	2.0	3476	9	ADC23395	Adc23395 Human CDN	C 364	47	2.0	7057	4	AA846601	Aas46601 Tumour su
292	48.2	2.0	3476	9	ADC26088	Adc26088 Human PRO	C 365	47	2.0	7057	6	ABL33848	Ab133848 Human imm
293	48.2	2.0	3476	9	ADE04915	Ade04915 Human PRO	C 366	47	2.0	7057	6	ABL34594	Ab134594 Human met
294	48.2	2.0	3476	9	ADE11221	Ade11221 Human PRO	C 367	47	2.0	7057	6	ABL70407	Ab170407 Chemicall
295	48.2	2.0	3476	9	ADB88152	ADB88152 Human PRO	C 368	47	2.0	7057	6	AAS61354	Aas61354 Human gen
296	48.2	2.0	3476	9	ADD95447	Add95447 Human CDN	C 369	47	2.0	11964	6	ABQ67025	Abq67025 Human ang
297	48.2	2.0	3476	9	ADE06377	Ade06377 Human PRO	C 370	47	2.0	16258	6	ABK40038	Abk40038 Human che
298	48.2	2.0	3476	9	ADE38152	Ade38152 Human PRO	C 371	47	2.0	16258	6	ABL70376	Ab170376 Chemicall
299	48.2	2.0	3476	9	ADD88268	Add88268 Human PRO	C 372	46.8	2.0	3153	4	AAF29464	Aaf29464 Murine br
300	48.2	2.0	3476	9	ADD90849	Add90849 Human CDN	C 373	46.8	2.0	3153	7	ACD66770	Acd66770 Secreted
301	48.2	2.0	3476	10	AD551702	Ad551702 Human CDN	C 374	46.8	2.0	3153	8	ADB90788	Adb90788 Mouse CDN
302	48.2	2.0	3476	10	AD551818	Ad551818 Human CDN	C 375	46.8	2.0	5987	6	ABL33563	Ab133563 Human imm
303	48.2	2.0	3476	10	AD37676	Ade37676 Human CDN	C 376	46.8	2.0	5987	6	ABQ67102	Abq67102 Human ang
304	48.2	2.0	3476	10	AD37560	Ade37560 Human CDN	C 377	46.8	2.0	5987	9	AD54180	Adb54180 Pretreate
305	48.2	2.0	3476	10	AD95331	Ad95331 Human CDN	C 378	46.8	2.0	5987	9	AD54308	Adb54308 Pretreate
306	48.2	2.0	3476	10	AD383031	Ade383031 Human PRO	C 379	46.8	2.0	6301	6	ABL32052	Ab132052 Human imm
307	48.2	2.0	3476	10	AD76120	Ade76120 Human PRO	C 380	46.8	2.0	9760	6	ABK31243	Abk31243 Signal tr
308	48.2	2.0	3476	10	AD39443	Ade39443 Human PRO	C 381	46.8	2.0	9760	6	AB170198	Ab170198 Chemicall
309	48.2	2.0	3476	10	AD804247	Ade04247 Human PRO	C 382	46.8	2.0	9760	6	AAS61156	Aas61156 Human gen
310	48.2	2.0	3476	10	AD39844	Ade39844 Human PRO	C 383	46.8	2.0	12968	4	AAS45494	Aas45494 Chemicall
311	48.2	2.0	3476	10	AD319709	Adel9709 Human PRO	C 384	46.8	2.0	12968	4	AAS46779	Aas46779 Tumour su
312	48.2	2.0	3476	10	AD77287	Ade77287 Human CDN	C 385	46.8	2.0	12968	6	ABL34085	Ab134085 Human imm
313	48.2	2.0	3476	10	AD65395	Ade65395 Human PRO	C 386	46.8	2.0	12968	6	ABK28424	Abk28424 DNA trans
314	48.2	2.0	3476	10	AD76004	Ade76004 Human PRO	C 387	46.8	2.0	12968	6	ABN80285	Abn80285 Human che
315	48.2	2.0	3476	10	AD37915	Ade37915 Human PRO	C 388	46.8	2.0	50000	6	ABL56202	Ab156202 AmEPV gen

C 389	46.6	2.0	315	3	AA02796	Human sec	C 462	45.6	1.9	11155	6	ABL32604	Human imm
C 390	46.6	2.0	883	4	Ad115210	Human bre	463	45.6	1.9	110000	6	ABA92787_1	Continuation (2 of
C 391	46.6	2.0	2000	7	AdA71938	Rice gene	464	45.4	1.9	6265	2	AA08523	BP46 (ro
C 392	46.6	2.0	2747	6	ABN86507	Rat glyco	465	45.4	1.9	7498	6	ABL32257	Human imm
C 393	46.6	2.0	3207	6	ABK63681	Rat seque	C 466	45.4	1.9	9881	6	ABL54354	Chemical
C 394	46.6	2.0	2747	2	AAQ14263	p-meta-1	C 467	45.4	1.9	10279	6	ABL33591	Human imm
C 395	46.6	2.0	5163	6	ABL33248	Human imm	C 468	45.4	1.9	10279	6	ABL92277	Chemical
C 396	46.6	2.0	7676	6	ABL34598	Human met	C 469	45.4	1.9	10279	6	AA022328	Chemical
C 397	46.6	2.0	7676	6	ABL70409	Chemical	C 470	45.4	1.9	11260	4	AA45315	Chemical
C 398	46.6	2.0	9180	6	ABL33964	Human imm	C 471	45.4	1.9	11260	6	AA828154	DNA trans
C 399	46.6	2.0	10891	6	ABL32465	Human imm	C 472	45.4	1.9	11260	6	ABN80039	Human che
C 400	46.6	2.0	11092	6	ABL33512	Human imm	C 473	45.4	1.9	11996	6	ABL34493	Human met
C 401	46.6	2.0	12507	6	ABL32298	Human imm	C 474	45.4	1.9	13420	6	ABL32917	Human imm
C 402	46.6	2.0	15548	6	ABL34155	Human imm	C 475	45.4	1.9	15649	6	ABL70543	Chemical
C 403	46.6	2.0	16228	6	ABL34073	Human imm	C 476	45.4	1.9	34548	6	ABL70604	Chemical
C 404	46.6	2.0	50000	6	ABL55643	AMEPV gen	C 477	45.4	1.9	40324	6	ABQ67149	Human ang
C 405	46.4	2.0	4092	4	AAH54899	S. epider	C 478	45.4	1.9	40681	6	ABA92787_6	Continuation (7 of
C 406	46.4	2.0	4172	6	ABL32714	Human imm	C 479	45.4	1.9	110000	6	ABA92787_5	Continuation (6 of
C 407	46.4	2.0	6040	6	ABL92301	Chemical	C 480	45.2	1.9	1939	2	AAQ34622	Cytosolic
C 408	46.4	2.0	6040	6	ABL49370	Human pol	C 481	45.2	1.9	1942	2	AAQ12540	GS3A prom
C 409	46.4	2.0	16228	6	ABL70459	Chemical	C 482	45.2	1.9	5267	6	ABQ67043	Human ang
C 410	46.4	2.0	16228	6	AA614424	Human gen	C 483	45.2	1.9	7508	6	ABK31206	Signal tr
C 411	46.4	2.0	17594	6	ABL34026	Human imm	C 484	45.2	1.9	7833	9	ABD54184	Pretreat
C 412	46.4	2.0	19131	4	AA546717	Tumour su	C 485	45.2	1.9	7833	9	ABD37769	Human che
C 413	46.2	1.9	4590	1	AA060472	Sequence	C 486	45.2	1.9	8876	6	ABL34076	Human imm
C 414	46.2	1.9	5880	4	AA546331	Tumour su	C 487	45.2	1.9	10710	6	ABN79996	Human che
C 415	46.2	1.9	5880	4	ABK28177	DNA trans	C 488	45.2	1.9	17183	6	ABL32487	Human imm
C 416	46.2	1.9	5981	6	ABL33763	Human imm	C 489	45.2	1.9	17419	4	AA545393	Chemical
C 417	46.2	1.9	6831	6	ABL33487	Human imm	C 490	45.2	1.9	17419	6	ABL33295	Human imm
C 418	46.2	1.9	7833	9	ABD54312	Pretreat	C 491	45.2	1.9	17419	6	ABL32328	DNA trans
C 419	46.2	1.9	7833	9	ABD37779	Human che	C 492	45	1.9	12142	6	ABL33673	Human imm
C 420	46.2	1.9	12507	6	ABL32299	Human imm	C 493	45	1.9	14987	6	ABL32630	Human imm
C 421	46.2	1.9	15743	6	ABK28396	DNA trans	C 494	45	1.9	18133	6	ABK40018	Human che
C 422	46.2	1.9	19380	6	AA61427	Human gen	C 495	45	1.9	18133	6	ABL32941	Human imm
C 423	46.2	1.9	23993	9	ABD37663	Human che	C 496	45	1.9	19659	6	ABL32766	Human imm
C 424	46.2	1.9	50000	6	ABL55643	AMEPV gen	C 497	45	1.9	26811	2	AA020253	Borrelia
C 425	46.2	1.9	115218	7	ACA64845	Human HNR	C 498	44.8	1.9	3101	2	AAQ20247	Sequence
C 426	46	1.9	3057	2	AA099555	Nucleic a	C 499	44.8	1.9	4661	6	ABQ67022	Human ang
C 427	46	1.9	4661	6	ABQ67021	Human ang	C 500	44.8	1.9	5593	6	ABL33161	Human imm
C 428	46	1.9	6113	6	ABL32430	Human imm	C 501	44.8	1.9	6759	6	ABL32738	Human imm
C 429	46	1.9	6113	6	ABL92204	Chemical	C 502	44.8	1.9	7231	6	ABL54323	Chemical
C 430	46	1.9	6113	6	ABL49313	Human pol	C 503	44.8	1.9	10048	6	ABQ67015	Human ang
C 431	46	1.9	9095	6	ABQ67062	Human ang	C 504	44.8	1.9	20579	6	ABQ67074	Human ang
C 432	46	1.9	9524	6	ABK39994	Human che	C 505	44.8	1.9	34548	6	ABL70603	Chemical
C 433	46	1.9	9524	6	ABL32839	Human imm	C 506	44.6	1.9	5979	4	AA545313	Chemical
C 434	46	1.9	14316	6	ABK31519	Signal tr	C 507	44.6	1.9	5979	6	ABK28152	DNA trans
C 435	46	1.9	14316	6	ABL70606	Chemical	C 508	44.6	1.9	6063	6	ABK28394	DNA trans
C 436	46	1.9	14316	6	AA561445	Human gen	C 509	44.6	1.9	6759	6	ABL32739	Human imm
C 437	46	1.9	15587	6	ABK31343	Signal tr	C 510	44.6	1.9	8905	2	AA020263	Borrelia
C 438	46	1.9	15587	6	ABL70304	Chemical	C 511	44.6	1.9	13784	4	AA545414	Human che
C 439	46	1.9	16217	6	ABL32625	Human imm	C 512	44.6	1.9	14649	4	AA545414	Chemical
C 440	46	1.9	21537	6	ABL33998	Human imm	C 513	44.6	1.9	14649	6	ABK28267	DNA trans
C 441	46	1.9	1132	3	AAF12929	Aspergill	C 514	44.6	1.9	16236	6	ABL33022	Human imm
C 442	45.8	1.9	5520	6	ABL33518	Human imm	C 515	44.6	1.9	16579	9	ABD54246	Pretreat
C 443	45.8	1.9	5659	6	ABL32374	Human imm	C 516	44.6	1.9	16579	9	ABD54246	Pretreat
C 444	45.8	1.9	5659	6	ABK32391	Human DNA	C 517	44.6	1.9	18283	6	ABL70502	Chemical
C 445	45.8	1.9	5659	6	ABL34486	Human met	C 518	44.6	1.9	18283	6	AA561363	Human gen
C 446	45.8	1.9	5659	7	ABD20366	Prostate	C 519	44.6	1.9	50000	6	ABL56201	AMEPV gen
C 447	45.8	1.9	5659	7	ABD484173	Human ren	C 520	44.6	1.9	96588	9	ADC85260	Human Ptp
C 448	45.8	1.9	6065	6	ABL32505	Human imm	C 521	44.6	1.9	96589	8	ADA02780	Human PTP
C 449	45.8	1.9	6072	6	ABL32030	Human imm	C 522	44.6	1.9	96589	9	ADB72518	Human PTP
C 450	45.8	1.9	6120	6	ABL32493	Human imm	C 523	44.6	1.9	159400	6	ABQ88126	Human ost
C 451	45.8	1.9	6361	6	ABL33140	Human imm	C 524	44.4	1.9	714	8	ADB09790	Alloiooc
C 452	45.8	1.9	7498	6	ABL32257	Human imm	C 525	44.4	1.9	1431	3	AAZ37082	DNA seque
C 453	45.8	1.9	7508	6	ABK31207	Signal tr	C 526	44.4	1.9	1501	7	ABZ10188	Haematopo
C 454	45.8	1.9	8093	7	ABZ10177	Haematopo	C 527	44.4	1.9	1501	7	ABE84162	Human lym
C 455	45.8	1.9	8093	9	ABD54267	Pretreat	C 528	44.4	1.9	1671	2	AAQ24134	50 KD sub
C 456	45.8	1.9	8093	9	ABE84189	Human lym	C 529	44.4	1.9	3410	7	ABZ59722	T. thermo
C 457	45.8	1.9	18218	6	ABL33949	Human imm	C 530	44.4	1.9	4993	6	ABL34102	Human imm
C 458	45.8	1.9	319608	3	AAH51601	Human chr	C 531	44.4	1.9	5798	6	ABL33666	Human imm
C 459	45.8	1.9	319608	3	AAH51601	Human chr	C 532	44.4	1.9	6123	6	ABL32820	Human imm
C 460	45.8	1.9	319608	3	AAH51601	Human chr	C 533	44.4	1.9	6239	6	ABK31185	Signal tr
C 461	45.6	1.9	6265	2	AA08523	BP46 (ro	C 534	44.4	1.9	6239	6	ABL70146	Chemical

535	44.4	1.9	6239	6	AAS61072	Aas61072 Human gen	608	44	1.9	8952	4	AAS46445	Aas46445 Tumour su
536	44.4	1.9	7168	6	ABL92231	Chemical	C 609	44	1.9	11964	6	ABQ67026	Human ang
537	44.4	1.9	7168	6	AAD22318	Chemical	C 610	44	1.9	13627	6	ABQ66975	Human imm
538	44.4	1.9	7189	6	ABN80026	Human che	C 611	44	1.9	17674	6	ABL33345	Human imm
539	44.4	1.9	8032	6	ABK31479	Signal tr	C 612	44	1.9	56153	4	AAS46794	Tumour su
540	44.4	1.9	8032	6	ABL70448	Chemical	C 613	44	1.9	95109	6	ABQ99654	Human mem
541	44.4	1.9	8032	6	AAS61409	Human gen	C 614	43.8	1.8	5487	6	ABL33598	Human imm
542	44.4	1.9	8305	6	ABL33568	Human imm	C 615	43.8	1.8	6127	6	ABL34448	Human met
543	44.4	1.9	8310	2	AAZ29911	cDNA enco	C 616	43.8	1.8	6127	6	ABL70119	Chemical
544	44.4	1.9	11049	6	ABL32668	Human imm	C 617	43.8	1.8	6233	4	AAS46497	Tumour su
545	44.4	1.9	11049	6	ABL92218	Chemical	C 618	43.8	1.8	6418	6	ABL32323	Human imm
546	44.4	1.9	11049	6	ABL49321	Human pol	C 619	43.8	1.8	6418	6	AAS61074	Human gen
547	44.4	1.9	11694	4	AAS46698	Tumour su	C 620	43.8	1.8	6811	6	ABL34541	Human met
548	44.4	1.9	16633	6	ABN79985	Human che	C 621	43.8	1.8	6811	6	ABL70264	Chemical
549	44.4	1.9	18283	6	ABL70501	Chemical	C 622	43.8	1.8	8093	7	ABZ10178	Haematopo
550	44.4	1.9	18283	6	AAS61362	Human gen	C 623	43.8	1.8	8093	9	ADB54268	Pretrate
551	44.4	1.9	34688	6	ABQ67060	Human ang	C 624	43.8	1.8	8093	9	ADB4190	Human lym
552	44.4	1.9	83391	6	ABQ67094	Human ang	C 625	43.8	1.8	8227	6	ABQ67126	Human ang
553	44.4	1.9	110000	8	ADB12064_09	Continuation (10 o	C 626	43.8	1.8	11996	6	ABL34492	Human met
554	44.2	1.9	697	4	AAS28824	Human imm	C 627	43.8	1.8	12237	6	ABL34358	Human imm
555	44.2	1.9	697	4	ABA6691	Human CDN	C 628	43.8	1.8	14861	6	ABL33194	Human imm
556	44.2	1.9	697	6	ABV84028	Human pol	C 629	43.8	1.8	14861	6	ABL70553	Chemical
557	44.2	1.9	697	9	ADB31549	Human CDN	C 630	43.8	1.8	14861	6	AAS61202	Human gen
558	44.2	1.9	731	2	AAQ31693	Real rest	C 631	43.8	1.8	14919	4	AAS46506	Tumour su
559	44.2	1.9	1351	2	AAZ17145	Human gen	C 632	43.8	1.8	15743	6	ABK28395	DNA trans
560	44.2	1.9	2000	6	ABZ17044	Arabidops	C 633	43.8	1.8	16724	6	ABL33090	Human imm
561	44.2	1.9	2000	7	ADA69322	Arabidops	C 634	43.8	1.8	16724	6	ABL34536	Human met
562	44.2	1.9	5349	6	ABL32341	Human imm	C 635	43.8	1.8	16724	6	ABL70259	Chemical
563	44.2	1.9	6012	6	ABK31370	Signal tr	C 636	43.8	1.8	17703	6	ABK39952	Human che
564	44.2	1.9	6012	6	ABL70327	Chemical	C 637	43.8	1.8	18154	6	ABL32254	Human imm
565	44.2	1.9	6012	6	AAS61274	Human gen	C 638	43.8	1.8	18154	6	ABL32254	Human imm
566	44.2	1.9	6109	6	ABL32326	Human imm	C 639	43.6	1.8	555	3	AAC66747	DNA marke
567	44.2	1.9	6109	6	AAS61077	Human gen	C 640	43.6	1.8	583	6	ABQ40113	Oligonuc
568	44.2	1.9	6131	6	ABL32890	Human imm	C 641	43.6	1.8	583	6	ABQ40112	Oligonuc
569	44.2	1.9	6147	6	ABK31353	Signal tr	C 642	43.6	1.8	1988	4	AAK03309	Human bra
570	44.2	1.9	6290	6	ABL33047	Human imm	C 643	43.6	1.8	3128	7	ABZ10164	Haematopo
571	44.2	1.9	7456	6	ABL33930	Human imm	C 644	43.6	1.8	5368	6	ABL34176	Human imm
572	44.2	1.9	7456	6	ABL92292	Chemical	C 645	43.6	1.8	5407	6	ABL34091	Human imm
573	44.2	1.9	7644	6	ABL32530	Human imm	C 646	43.6	1.8	5511	6	ABL33870	Human imm
574	44.2	1.9	8093	4	AAS46435	Tumour su	C 647	43.6	1.8	6028	9	ADE84206	Human lym
575	44.2	1.9	8093	6	ABK33973	Human DNA	C 648	43.6	1.8	6106	4	AAS46430	Tumour su
576	44.2	1.9	8093	6	ABL92236	Chemical	C 649	43.6	1.8	6106	6	ABK40032	Human che
577	44.2	1.9	8093	6	ABL49331	Human MLH	C 650	43.6	1.8	6106	6	ABL33473	Human imm
578	44.2	1.9	8093	7	ABZ10031	Haematopo	C 651	43.6	1.8	6107	6	ABL70354	Chemical
579	44.2	1.9	8093	7	ADA20360	Prostate	C 652	43.6	1.8	6107	6	AAS61315	Human gen
580	44.2	1.9	8093	7	ADA84167	Human ren	C 653	43.6	1.8	6126	4	AAS46574	Tumour su
581	44.2	1.9	8093	7	ADB54139	Pretrate	C 654	43.6	1.8	6126	6	ABL33831	Human imm
582	44.2	1.9	8093	9	ADE84113	Human lym	C 655	43.6	1.8	6161	6	ABL32623	Human imm
583	44.2	1.9	9117	6	ABL33068	Human imm	C 656	43.6	1.8	6227	6	ABL33586	Human imm
584	44.2	1.9	9515	4	AAS45453	Chemical	C 657	43.6	1.8	6227	6	ABL92260	Chemical
585	44.2	1.9	9515	6	ABK28308	DNA trans	C 658	43.6	1.8	6459	7	ABZ79546	Radish Rf
586	44.2	1.9	9515	6	ABN80245	Human che	C 659	43.6	1.8	6558	4	AAK86101	Human imm
587	44.2	1.9	11187	6	ABK28452	DNA trans	C 660	43.6	1.8	6558	4	AAAL37138	Human mus
588	44.2	1.9	18283	6	ABL70501	Chemical	C 661	43.6	1.8	6558	5	ABA21372	Human ner
589	44.2	1.9	18283	6	AAS61362	Human gen	C 662	43.6	1.8	6558	7	ABX60126	cDNA enco
590	44.2	1.9	33053	6	ABQ67006	Human ang	C 663	43.6	1.8	7131	6	ABK31451	Signal tr
591	44	1.9	419	7	ABX46069	Bovine ES	C 664	43.6	1.8	7131	6	ABL70428	Chemical
592	44	1.9	3007	4	AAS45511	Chemical	C 665	43.6	1.8	7131	6	AAS61361	Human gen
593	44	1.9	3007	6	ABK28445	DNA trans	C 666	43.6	1.8	7143	6	ABL32982	Human imm
594	44	1.9	3151	6	ABQ67144	Human ang	C 667	43.6	1.8	7503	6	ABL33775	Human imm
595	44	1.9	3750	7	AAD48465	Brassica	C 668	43.6	1.8	7833	9	ADB54312	Pretrate
596	44	1.9	5820	6	ABL32538	Human imm	C 669	43.6	1.8	7833	9	AD337779	Human che
597	44	1.9	6129	6	ABK31237	Signal tr	C 670	43.6	1.8	8866	4	NAS45432	Chemical
598	44	1.9	6129	6	ABL70538	Chemical	C 671	43.6	1.8	8866	6	ABK28279	DNA trans
599	44	1.9	6129	6	AAS61150	Human gen	C 672	43.6	1.8	10467	6	ABK28453	DNA trans
600	44	1.9	6223	6	AAS61176	Human gen	C 673	43.6	1.8	10467	9	ADB54222	Pretrate
601	44	1.9	6306	4	AAS45422	Chemical	C 674	43.6	1.8	12507	6	ABL32299	Human imm
602	44	1.9	6437	6	ABL33260	Human imm	C 675	43.6	1.8	13326	6	ABL33712	Human imm
603	44	1.9	7321	6	ABK31424	Signal tr	C 676	43.6	1.8	13503	6	ABL34070	Human imm
604	44	1.9	7321	6	ABL70385	Chemical	C 677	43.6	1.8	14537	4	AAS46356	Tumour su
605	44	1.9	7321	6	AAS61337	Human gen	C 678	43.6	1.8	16173	6	ABL34469	Human met
606	44	1.9	7522	6	ABL32914	Human imm	C 679	43.6	1.8	18624	6	ABL33702	Human imm
607	44	1.9	7597	6	ABL33013	Human imm	C 680	43.6	1.8	19734	6	ABL33933	Human imm

c 681	43.6	1.8	47108	6	ABK31510	Abk31510 Signal tr
c 682	43.6	1.8	50000	6	ABL55644	Abi155644 AmEPV gen
c 683	43.6	1.8	83391	6	ABQ67093	Abq67093 Human ang
c 684	43.4	1.8	337	7	ABX41811	Abx41811 Bovine ES
c 685	43.4	1.8	547	6	ABQ14987	Abq14987 Oligonuclei
c 686	43.4	1.8	547	6	ABQ14986	Abq14986 Oligonuclei
c 687	43.4	1.8	830	6	ABQ89354	Abq89354 Human prn
c 688	43.4	1.8	830	6	ABQ82297	Abq82297 Human cDN
c 689	43.4	1.8	2196	6	ABi199480	Abi199480 Mouse lsc
c 690	43.4	1.8	5376	6	ABL34150	Abi34150 Human imm
c 691	43.4	1.8	6012	6	ABK31491	Abk31491 Signal tr
c 692	43.4	1.8	6012	6	ABL70464	Abi70464 Chemical
c 693	43.4	1.8	6106	4	AAS46430	Aas46430 Tumour su
c 694	43.4	1.8	6106	6	ABK40032	Abk40032 Human che
c 695	43.4	1.8	6106	6	ABL33473	Abi33473 Human imm
c 696	43.4	1.8	6317	6	ABL32408	Abi32408 Human imm
c 697	43.4	1.8	6317	6	ABL49311	Abi49311 Human pol
c 698	43.4	1.8	6585	6	ABL32832	Abi32832 Human imm
c 699	43.4	1.8	6585	6	AAS61182	Aas61182 Human gen
c 700	43.4	1.8	6590	6	ABL33476	Abi33476 Human imm
c 701	43.4	1.8	6942	6	ABL33735	Abi33735 Human imm
c 702	43.4	1.8	7903	4	AAS45403	Aas45403 Chemical
c 703	43.4	1.8	7903	6	ABL33363	Abi33363 Human imm
c 704	43.4	1.8	7903	6	ABK28248	Abk28248 DNA trans
c 705	43.4	1.8	8222	7	ACF62816	Acf62816 Colon can
c 706	43.4	1.8	8222	7	ACF62794	Acf62794 Colon can
c 707	43.4	1.8	9021	6	ABK40075	Abk40075 Human che
c 708	43.4	1.8	9021	6	ABL34232	Abi34232 Human imm
c 709	43.4	1.8	9021	6	ABK33988	Abk33988 Human DNA
c 710	43.4	1.8	9021	7	ADA20388	Ada20388 Prostate
c 711	43.4	1.8	9021	7	ADA84195	Ada84195 Human ren
c 712	43.4	1.8	11222	9	ADB54190	Adb54190 Pretreat
c 713	43.4	1.8	11222	9	ADB54318	Adb54318 Pretreat
c 714	43.4	1.8	11422	6	ABK39937	Abk39937 Human che
c 715	43.4	1.8	11422	6	ABL32219	Abi32219 Human imm
c 716	43.4	1.8	13427	6	ABL33927	Abi33927 Human imm
c 717	43.4	1.8	17137	6	ABL32190	Abi32190 Human imm
c 718	43.4	1.8	24939	6	ABL70570	Abi70570 Chemical
c 719	43.4	1.8	40324	6	ABQ67150	Abq67150 Human ang
c 720	43.4	1.8	90541	6	ABS52847	Abs52847 Human SR
c 721	43.4	1.8	113033	7	ABL54213	Abi54213 SR protei
c 722	43.2	1.8	469	5	ABV56638	Abv56638 Human pro
c 723	43.2	1.8	1982	2	AAV40736	Aav40736 C. felis
c 724	43.2	1.8	1982	2	AAV40735	Aav40735 C. felis
c 725	43.2	1.8	1982	4	AAD21167	Aad21167 Ctenoceph
c 726	43.2	1.8	2144	2	AAV40758	Aav40758 C. felis
c 727	43.2	1.8	2144	2	AAV40759	Aav40759 C. felis
c 728	43.2	1.8	2144	4	AAD21182	Aad21182 Ctenoceph
c 729	43.2	1.8	2501	9	ADB54116	Adb54116 Pretreat
c 730	43.2	1.8	2652	7	ABZ81728	Abz81728 Rat brain
c 731	43.2	1.8	2652	7	ABZ81727	Abz81727 Rat mutan
c 732	43.2	1.8	3077	9	ADB59097	Adb59097 Toxicity-
c 733	43.2	1.8	5294	6	ABL33070	Abi33070 Human imm
c 734	43.2	1.8	5294	6	ABK31282	Abk31282 Signal tr
c 735	43.2	1.8	6042	3	AAA70199	Aaa70199 Plasmodi
c 736	43.2	1.8	6095	4	AAS46310	Aas46310 Tumour su
c 737	43.2	1.8	6095	6	ABL32361	Abi32361 Human imm
c 738	43.2	1.8	6095	6	ABL34475	Abi34475 Human met
c 739	43.2	1.8	6095	6	ABL70150	Abi70150 Chemical
c 740	43.2	1.8	6285	6	ABL33496	Abi33496 Human imm
c 741	43.2	1.8	6286	4	AAS46591	Aas46591 Tumour su
c 742	43.2	1.8	6641	6	ABL32315	Abi32315 Human imm
c 743	43.2	1.8	6641	6	ABL54336	Abi54336 Chemical
c 744	43.2	1.8	6880	6	ABK31323	Abk31323 Signal tr
c 745	43.2	1.8	6880	6	ABi70294	Abi70294 Chemical
c 746	43.2	1.8	6880	6	AAS61224	Aas61224 Human gen
c 747	43.2	1.8	10710	6	ABL32893	Abi32893 Human imm
c 748	43.2	1.8	11670	6	ABL54326	Abi54326 Chemical
c 749	43.2	1.8	13712	6	ABL33531	Abi33531 Human imm
c 750	43.2	1.8	14307	6	ABL32729	Abi32729 Human imm
c 751	43.2	1.8	15373	6	ABL32467	Abi32467 Human imm
c 752	43.2	1.8	16217	6	ABL32625	Abi32625 Human imm
c 753	43.2	1.8	17594	6	ABL34027	Abi34027 Human imm
c 754	43.2	1.8	20674	3	AAC58017	Aac58017 Arachidon
c 755	43.2	1.8	24939	6	ABL70570	Abi70570 Chemical
c 756	43.2	1.8	74586	6	AAS16905	Aas16905 Genomic D
c 757	43	1.8	1132	6	ABZ15647	Abz15647 Arabidops
c 758	43	1.8	5218	6	ABL33266	Abi33266 Human imm
c 759	43	1.8	5942	6	ABK33945	Abk33945 Human DNA
c 760	43	1.8	5942	6	ABK31223	Abk31223 Signal tr
c 761	43	1.8	5942	6	ABL70534	Abi70534 Chemical
c 762	43	1.8	5942	6	AAS61135	Aas61135 Human gen
c 763	43	1.8	5942	7	ABZ10002	Abz10002 Haematopo
c 764	43	1.8	5942	7	ABZ10234	Abz10234 Haematopo
c 765	43	1.8	5942	7	ABZ10088	Abz10088 Haematopo
c 766	43	1.8	5942	7	ABZ10148	Abz10148 Haematopo
c 767	43	1.8	5942	7	ADA20351	Ada20351 Prostate
c 768	43	1.8	5942	7	ADA84158	Ada84158 Human ren
c 769	43	1.8	5942	9	ADE84068	Ade84068 Human lym
c 770	43	1.8	5942	9	ADE84144	Ade84144 Human lym
c 771	43	1.8	6077	6	ABL33246	Abi33246 Human imm
c 772	43	1.8	6126	4	AAS46573	Aas46573 Tumour su
c 773	43	1.8	6233	6	ABL33830	Abi33830 Human imm
c 774	43	1.8	6233	6	AAS46498	Aas46498 Tumour su
c 775	43	1.8	6317	6	ABL32409	Abi32409 Human imm
c 776	43	1.8	6317	6	ABL49312	Abi49312 Human pol
c 777	43	1.8	7441	6	ABK40057	Abk40057 Human che
c 778	43	1.8	7479	6	AAS63344	Aas63344 Chemical
c 779	43	1.8	7900	4	AAS46760	Aas46760 Tumour su
c 780	43	1.8	8592	6	ABL33983	Abi33983 Human imm
c 781	43	1.8	9810	6	ABL32427	Abi32427 Human imm
c 782	43	1.8	11787	6	ABL92243	Abi92243 Chemical
c 783	43	1.8	11787	9	ADB54202	Adb54202 Pretreat
c 784	43	1.8	13574	6	ABL33316	Abi33316 Human imm
c 785	43	1.8	16228	6	ABL70459	Abi70459 Chemical
c 786	43	1.8	16228	6	AAS61424	Aas61424 Human gen
c 787	43	1.8	16579	9	ADB54118	Adb54118 Pretreat
c 788	43	1.8	18579	9	ABE37763	Abe37763 Human che
c 789	43	1.8	19082	6	ABL32627	Abi32627 Human imm
c 790	43	1.8	19082	6	ABL32627	Abi32627 Human imm
c 791	43	1.8	20933	9	ABQ67124	Abq67124 Human ang
c 792	43	1.8	29993	9	ABD37661	Abd37661 Human che
c 793	43	1.8	37184	6	ABQ67078	Abq67078 Human ang
c 794	43	1.8	38342	4	AAS46746	Aas46746 Tumour su
c 795	43	1.8	38342	4	ABK31507	Abk31507 Signal tr
c 796	43	1.8	50000	6	ABL56202	Abi56202 AmEPV gen
c 797	42.8	1.8	2000	6	ABZ16071	Abz16071 Arabidops
c 798	42.8	1.8	5204	6	ABL32899	Abi32899 Human imm
c 799	42.8	1.8	5454	3	AAA70236	Aaa70236 Plasmodi
c 800	42.8	1.8	5611	6	ABQ67069	Abq67069 Human ang

ALIGNMENTS

RESULT 1

AAK52250

ID AAK52250 standard; DNA; 2372 BP.

XX

AC AAK52250;

XX

DT 25-JUN-1999 (first entry)

XX Protein PRO263 cDNA clone DNA34431-1171.

DE Secreted protein; transmembrane protein; human; enterocolitis;

XX Zollinger-Ellison syndrome; gastrointestinal ulceration;

KW congenital microvillus atrophy; skin disease; cell growth;

KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;

KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;

KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;

KW wound healing; tissue repair; ss.

XX Homo sapiens.

OS WO9914328-A2.

PN

QY 781 GAAACTAGCACCATGCTACAGAAACTGAACCAATTTGTTGAAAAATAAAGCAGCATTCAAG 840
Db |||||
QY 781 GAACTAGCACCATGCTACAGAAACTGAACCAATTTGTTGAAAAATAAAGCAGCATTCAAG 840
Db |||||
QY 841 AATGAAGCTGTGGGTTTGGAGGTGTCGCCAGGCTCTGCTAGTGTCTCTCTCTTC 900
Db |||||
QY 841 AATGAAGCTGTGGGTTTGGAGGTGTCGCCAGGCTCTGCTAGTGTCTCTCTCTTC 900
Db |||||
QY 901 TTTGGTGTGCTGAGCTGGTCTTGATTTTGGATTTGCTATGTCACAAAGGTATGTAAGGCTTCCCT 960
Db |||||
QY 901 TTTGGTGTGCTGAGCTGGTCTTGATTTTGGATTTGCTATGTCACAAAGGTATGTAAGGCTTCCCT 960
Db |||||
QY 961 TTTTCAAAACAAGAAATCAGCAGAAAGAAATGATCGAAACCAAGTAGTAAAGGAGAGAG 1020
Db |||||
QY 961 TTTTCAAAACAAGAAATCAGCAGAAAGAAATGATCGAAACCAAGTAGTAAAGGAGAGAG 1020
Db |||||
QY 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAACTGATATAAAACCCAGAGAGTCC 1080
Db |||||
QY 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAACTGATATAAAACCCAGAGAGTCC 1080
Db |||||
QY 1081 AAGAGTCCAAAGCAAACTACCGTGGATGCGGATGCTGGAGCTGAAGTTAGATGAGACAGAAA 1140
Db |||||
QY 1081 AAGAGTCCAAAGCAAACTACCGTGGATGCGGATGCTGGAGCTGAAGTTAGATGAGACAGAAA 1140
Db |||||
QY 1141 TGAGGAGACACACCTGAGGCTGTTCTTTTATGCTCTCTTACCTGCCCCAGCTGGGAA 1200
Db |||||
QY 1141 TGAGGAGACACACCTGAGGCTGTTCTTTTATGCTCTCTTACCTGCCCCAGCTGGGAA 1200
Db |||||
QY 1201 ATCAAAAGGGGCAAGAAAGCAAGAAAGAAAGTCCACCTTGGTCTTAACTGGAATCAGC 1260
Db |||||
QY 1201 ATCAAAAGGGGCAAGAAAGCAAGAAAGAAAGTCCACCTTGGTCTTAACTGGAATCAGC 1260
Db |||||
QY 1261 TCAGGACTGCATTTGATGCTATGCTGCTGACCAAGAGATGCTCTTCTCTTATTTAAAC 1320
Db |||||
QY 1261 TCAGGACTGCATTTGATGCTATGCTGCTGACCAAGAGATGCTCTTCTCTTATTTAAAC 1320
Db |||||
QY 1321 CCTGTCTGGATCTCTATCTCTTACCTCCAAAGCTTCCACGCGCTTTCTAGCTGGCTAT 1380
Db |||||
QY 1321 CCTGTCTGGATCTCTATCTCTTACCTCCAAAGCTTCCACGCGCTTTCTAGCTGGCTAT 1380
Db |||||
QY 1381 GTCTTAATAATATCCACTGGGAGAAAGAGTGTGCAAGTGCAGGACCTTAAACATC 1440
Db |||||
QY 1381 GTCTTAATAATATCCACTGGGAGAAAGAGTGTGCAAGTGCAGGACCTTAAACATC 1440
Db |||||
QY 1441 TCATCAGTATCCAGTGTGAAAAGGCTCTGCTGCTGCTGAGGCTAGTGGTGAAGC 1500
Db |||||
QY 1441 TCATCAGTATCCAGTGTGAAAAGGCTCTGCTGCTGCTGAGGCTAGTGGTGAAGC 1500
Db |||||
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCTTTCTTCA 1560
Db |||||
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCTTTCTTCA 1560
Db |||||
QY 1561 GCTCTGAAGAGAAACAGATATCCACTGATGCTCTCTGAGCCGGTAAAGGAAA 1620
Db |||||
QY 1561 GCTCTGAAGAGAAACAGATATCCACTGATGCTCTCTGAGCCGGTAAAGGAAA 1620
Db |||||
QY 1621 AGAATGGCAGAAAAGTTTGTAGCCCTGAAAGCCATGAGATCTCTAATCTTGAGACCTAA 1680
Db |||||
QY 1621 AGAATGGCAGAAAAGTTTGTAGCCCTGAAAGCCATGAGATCTCTAATCTTGAGACCTAA 1680
Db |||||
QY 1681 TCTCTGTAAGCTAAATAAAGAAATAGAAACCAAGGCTGAGGATACGACAGTACATGTCA 1740
Db |||||
QY 1681 TCTCTGTAAGCTAAATAAAGAAATAGAAACCAAGGCTGAGGATACGACAGTACATGTCA 1740
Db |||||
QY 1741 GCAGGACTGTAAACACAGACAGGCTCAAGTGTCTCTGTAACACATTTGAGTTGGAAT 1800
Db |||||
QY 1741 GCAGGACTGTAAACACAGACAGGCTCAAGTGTCTCTGTAACACATTTGAGTTGGAAT 1800
Db |||||
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACACCTGCTGATATTTCTCT 1860
Db |||||
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACACCTGCTGATATTTCTCT 1860
Db |||||

QY 1861 AGGAAATATACCTTTTACAAAGTAACAAAATAAAAACTCTTATAAATTTCTATTATCT 1920
Db |||||
QY 1861 AGGAAATATACCTTTTACAAAGTAACAAAATAAAAACTCTTATAAATTTCTATTATCT 1920
Db |||||
QY 1921 GAGTTACAGAAATGATTTACTAAGGAGATTTACTCAGTAATTTGTTTAAAAAGTATAAAA 1980
Db |||||
QY 1921 GAGTTACAGAAATGATTTACTAAGGAGATTTACTCAGTAATTTGTTTAAAAAGTATAAAA 1980
Db |||||
QY 1981 TTTCAACAAACATTTTGTCTGAATAGCTTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040
Db |||||
QY 1981 TTTCAACAAACATTTTGTCTGAATAGCTTACTATATGTCAAGTGTGTGCAAGGTATTACACTC 2040
Db |||||
QY 2041 TGTAAATGAAATATTATTTCTTCAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
Db |||||
QY 2041 TGTAAATGAAATATTATTTCTTCAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
Db |||||
QY 2101 TTTTTCAGTTTGTATTTTCTAGCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2160
Db |||||
QY 2101 TTTTTCAGTTTGTATTTTCTAGCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2160
Db |||||
QY 2161 GACTAATCTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2220
Db |||||
QY 2161 GACTAATCTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2220
Db |||||
QY 2221 ATACCTAAGAGTACATTTGTTTACCTCTATATACCAAGACATTTTAAAAAGTGCATTA 2280
Db |||||
QY 2221 ATACCTAAGAGTACATTTGTTTACCTCTATATACCAAGACATTTTAAAAAGTGCATTA 2280
Db |||||
QY 2281 CAATGTATCTACTAGCCCTCTTTTCCAAAGAGGAGCTGAGAGATGCAAGATATT 2340
Db |||||
QY 2281 CAATGTATCTACTAGCCCTCTTTTCCAAAGAGGAGCTGAGAGATGCAAGATATT 2340
Db |||||
QY 2341 TGTGCAAAAAATTTAAAGCATTTTAAAGAACTT 2372
Db |||||
QY 2341 TGTGCAAAAAATTTAAAGCATTTTAAAGAACTT 2372
Db |||||

RESULT 2

ADC78520

ID ADC78520 standard; cdna; 2372 BP.

XX AC ADC78520;

XX DT 01-JAN-2004 (first entry)

XX DE Human PRO263 cdna.

XX KW antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
nootropic; neuroprotective; vasotropic; chemotactic; angiogenic;
neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
antiarteriosclerotic; cardiac; antidiabetic; cerebroprotective;
thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.

XX OS Homo sapiens.

XX PN WO200015796-A2.

XX PD 23-MAR-2000.

XX PF 15-SEP-1999; 99WO-US021090.

XX PR 16-SEP-1998; 98WO-US019330.

XX PA (GETH) GENENTECH INC.

XX PI Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;

PI Yuan J;

Db 1741 GCAGGAGCTGTAAACACACACAGCGGTCAAAGTGTCTTCTCTGAACACATTTGAGTTGGAAT 1800
Qy 1801 CACTGTTTAAAGACACACACACTTACTTTTCTGGTCTCTACACCTGCTGATATTTCTCT 1860
Db 1801 CACTGTTTAAAGACACACACACTTACTTTTCTGGTCTCTACACCTGCTGATATTTCTCT 1860
Qy 1861 AGGAAATATCTTTTACAAAGTAACAAAATATAAACTCTTATAAATTTCTATTTTATCT 1920
Db 1861 AGGAAATATCTTTTACAAAGTAACAAAATATAAACTCTTATAAATTTCTATTTTATCT 1920
Qy 1921 GAGTTACAGAAATGATTTACTAAGGAAGTACTCAGTAATTTGTTTAAAAAGTATAAAA 1980
Db 1921 GAGTTACAGAAATGATTTACTAAGGAAGTACTCAGTAATTTGTTTAAAAAGTATAAAA 1980
Qy 1981 TTCAACAAACATTTGCTCAATAGCTACTATATGTCAAGTGTCTGCAAGGTATTACACTC 2040
Db 1981 TTCAACAAACATTTGCTCAATAGCTACTATATGTCAAGTGTCTGCAAGGTATTACACTC 2040
Qy 2041 TGTAAATGAAATATTCTCTCAAAAATTTGCACATAGTAGAAGCGCTATCTGGGAAGCTAT 2100
Db 2041 TGTAAATGAAATATTCTCTCAAAAATTTGCACATAGTAGAAGCGCTATCTGGGAAGCTAT 2100
Qy 2101 TTTTTCAGTTTGTATATTTCTAGCTTATCTACTTCCAACTAATTTTATTTTGTCTGA 2160
Db 2101 TTTTTCAGTTTGTATATTTCTAGCTTATCTACTTCCAACTAATTTTATTTTGTCTGA 2160
Qy 2161 GACTAATCTTATTCATTTTCTTAATATGCAACCAATTAACCTTAATTTATTTAATTAAC 2220
Db 2161 GACTAATCTTATTCATTTTCTTAATATGCAACCAATTAACCTTAATTTATTTAATTAAC 2220
Qy 2221 ATACTAAGAAGTACATTTGTTACCTCTATATACCAAGCACATTTTAAAAAGTGCCATTAA 2280
Db 2221 ATACTAAGAAGTACATTTGTTACCTCTATATACCAAGCACATTTTAAAAAGTGCCATTAA 2280
Qy 2281 CAATGTATCTAGTACCTCTCTTTTCCAAAGAGGAGCTGAGATGCGAATAATTT 2340
Db 2281 CAATGTATCTAGTACCTCTCTTTTCCAAAGAGGAGCTGAGATGCGAATAATTT 2340
Qy 2341 TGTGACAAAAATTAAGCAATTTAGAAAACCTT 2372
Db 2341 TGTGACAAAAATTAAGCAATTTAGAAAACCTT 2372

RESULT 3
AAF72408
ID AAF72408 standard; cDNA; 2372 BP.
XX
AC AAF72408;
XX
DT 24-APR-2001 (first entry)
XX
DE Human PR0263 cDNA.
XX
KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnery; cardiant;
KW angiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antithalctic; antiinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmologic; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200104311-A1.
XX
PD 18-JAN-2001.
XX
PF 22-FEB-2000; 2000WO-US004414.
XX
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
XX
XX (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin LJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI; 2001-081051/09.
DR P-PSDB; AAB80247.
XX
XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT disease).
XX
PS Claim 2; Fig 73; 393pp; English.
XX
CC The present sequence is one of sixty one nucleic acids encoding novel
CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are
CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
CC squamous cell carcinoma), gastrointestinal disorders (e.g.
CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
CC endometrial bleeding, angiogenesis, ischaemias such as coronary ischaemia,
CC atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid
CC arthritis, multiple sclerosis), infertility, AIDS and diabetes and
CC retinal disorders such as retinitis pigmentosa. The PRO nucleic acids
CC have applications in molecular biology, including use as hybridization
CC probes, and in chromosome and gene mapping
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCAGGGAATCCGGATGTCCTCGGTTATGAAAGTGAGCAGTGAGTGTGAGCCTCAACATA 60
Db 1 AGCAGGGAATCCGGATGTCCTCGGTTATGAAAGTGAGCAGTGAGTGTGAGCCTCAACATA 60
Qy 61 GTTCAGAACTCTCCATCCGAGCTAGTTATTGAGCATCTGCTCTCATATCACAGTGGC 120
Db 61 GTTCAGAACTCTCCATCCGAGCTAGTTATTGAGCATCTGCTCTCATATCACAGTGGC 120
Qy 121 CATCTGAGCTGTTCCCTGGCTCTGAAGGGGTAGGCAGATGGCCAGGTGTTTCAGCCTG 180
Db 121 CATCTGAGCTGTTCCCTGGCTCTGAAGGGGTAGGCAGATGGCCAGGTGTTTCAGCCTG 180
Qy 181 GTTGTGCTTCTCACTTCCATCTGGACCAAGGCTCTCTGGTCCAAGGCTCTTTTGGTGCA 240
Db 181 GTTGTGCTTCTCACTTCCATCTGGACCAAGGCTCTCTGGTCCAAGGCTCTTTTGGTGCA 240
Qy 241 GAAGAGCTTTCCATCCAGGTGTCATGAGAAATTTATGGGATCACCTCTGTGAGCAAAAG 300
Db 241 GAAGAGCTTTCCATCCAGGTGTCATGAGAAATTTATGGGATCACCTCTGTGAGCAAAAG 300
Qy 301 GCGAACACAGCAGCTGAATTTACAGAGCTAAGAGGCTGTAGGCTGTCTGGACTAAGT 360
Db 301 GCGAACACAGCAGCTGAATTTACAGAGCTAAGAGGCTGTAGGCTGTCTGGACTAAGT 360

QY 361 TTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
 Db 361 TTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
 QY 421 GGCTGGGTTGGAGATGGAATTCGTGGTCACTCTCTAGGATTAAGCCCAAAACCCCAAGTGTGGG 480
 Db 421 GGCTGGGTTGGAGATGGAATTCGTGGTCACTCTCTAGGATTAAGCCCAAAACCCCAAGTGTGGG 480
 QY 481 AAAAAATGGGTTGGGTTGCTGATTTGGAAGTTTCAGTGGCCGACAGTTTGAAGCCCTAT 540
 Db 481 AAAAAATGGGTTGGGTTGCTGATTTGGAAGTTTCAGTGGCCGACAGTTTGAAGCCCTAT 540
 QY 541 TGTATCAACTCATCTGATACCTGACATACTCGTGCAATTCAGAGAAATTAATCACCACCAAA 600
 Db 541 TGTATCAACTCATCTGATACCTGACATACTCGTGCAATTCAGAGAAATTAATCACCACCAAA 600
 QY 601 GATCCCATATTCACACATCAAACTGCAACACAAACAAACAGAAATTAATGTCAGTGACAGT 660
 Db 601 GATCCCATATTCACACATCAAACTGCAACACAAACAAACAGAAATTAATGTCAGTGACAGT 660
 QY 661 ACCTACTCGGTGGCATCCCTTACTCTACATACCTGCCCCCTACTACTCTCCTGCT 720
 Db 661 ACCTACTCGGTGGCATCCCTTACTCTACATACCTGCCCCCTACTACTCTCCTGCT 720
 QY 721 CCAGCTTCCACTTCTATTTCCACGAGAGAAAAAATTTGATTTGTGTCACAGAAATTTTATG 780
 Db 721 CCAGCTTCCACTTCTATTTCCACGAGAGAAAAAATTTGATTTGTGTCACAGAAATTTTATG 780
 QY 781 GAAACTAGCACCATGTCACAGAAACTGAAACCAATTTGTTGAAATAAAGCAGCAATTCAG 840
 Db 781 GAAACTAGCACCATGTCACAGAAACTGAAACCAATTTGTTGAAATAAAGCAGCAATTCAG 840
 QY 841 AATGAGCTGCTGGGTTTGGAGTGTCCACAGCTCTGCTAGTGTCTCTCTCTTC 900
 Db 841 AATGAGCTGCTGGGTTTGGAGTGTCCACAGCTCTGCTAGTGTCTCTCTCTTC 900
 QY 901 TTTGGTCTGCGCTGCTTTGGAATTTGCTATGTCACAAAGGATGTGGAAGGCTTCCCT 960
 Db 901 TTTGGTCTGCGCTGCTTTGGAATTTGCTATGTCACAAAGGATGTGGAAGGCTTCCCT 960
 QY 961 TTTTCAAAACGAATCAGCAGAGGAAATGATCGAAACCAAGATGATAGGAGGAGAG 1020
 Db 961 TTTTCAAAACGAATCAGCAGAGGAAATGATCGAAACCAAGATGATAGGAGGAGAG 1020
 QY 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAACCTAAGAGTAAAGGAGGAGATC 1080
 Db 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAACCTAAGAGTAAAGGAGGAGATC 1080
 QY 1081 AAGAGTCCAAAGCAAACTACCGTGGATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140
 Db 1081 AAGAGTCCAAAGCAAACTACCGTGGATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140
 QY 1141 TGAGGAGACACACTGAGGTGGTTCTTTTATGCTCTCTTACCTGCCCCCAGCTGGGAA 1200
 Db 1141 TGAGGAGACACACTGAGGTGGTTCTTTTATGCTCTCTTACCTGCCCCCAGCTGGGAA 1200
 QY 1201 ATCAAAAGGCCAAAGNACCAAGAGAAAGTCCACCTTGGTCTTAACTGGAATCAGC 1260
 Db 1201 ATCAAAAGGCCAAAGNACCAAGAGAAAGTCCACCTTGGTCTTAACTGGAATCAGC 1260
 QY 1261 TCAGGACTGCCATGGACTATGGAGTGCACCAAGAGAAATGCTCTCTCTTATTTGAAC 1320
 Db 1261 TCAGGACTGCCATGGACTATGGAGTGCACCAAGAGAAATGCTCTCTCTTATTTGAAC 1320
 QY 1321 CCTGTCTGATCTTACTCTCTCAAGCTTCCACGGCTTTCTAGCCTGGCTAT 1380
 Db 1321 CCTGTCTGATCTTACTCTCTCAAGCTTCCACGGCTTTCTAGCCTGGCTAT 1380
 QY 1381 GTCTTAATATATCCCACTGGGAGAAAGGAGTTTGGAAAGTGAAGGACCTTAAACATC 1440
 Db 1381 GTCTTAATATATCCCACTGGGAGAAAGGAGTTTGGAAAGTGAAGGACCTTAAACATC 1440
 QY 1441 TCATCAGTATCCAGTGTGTAAGAGGCTCTCTGGCTGTCTGAGGCTAGTGGGTTGAAAGC 1500

Db 1441 TCATCAGTATCCAGTGTGTAAGAGGCTCTCTGGCTGTCTGAGGCTAGTGGGTTGAAAGC 1500
 QY 1501 CAAGGACTCACTGAGACCAAGGCTTTCTTACTGATTTCCGAGCTCAGACCTTTCTTCA 1560
 Db 1501 CAAGGACTCACTGAGACCAAGGCTTTCTTACTGATTTCCGAGCTCAGACCTTTCTTCA 1560
 QY 1561 GCTCTGAAAGAGAAACAGCTATCCACCTGACATGCTCTTCTGAGCCCGGTAAGAGCAA 1620
 Db 1561 GCTCTGAAAGAGAAACAGCTATCCACCTGACATGCTCTTCTGAGCCCGGTAAGAGCAA 1620
 QY 1621 AGAATGCGCAGAAAGTTTAGCCCTGAAAGCCATGAGATTTCTCATCTTGTGAGACCTAA 1680
 Db 1621 AGAATGCGCAGAAAGTTTAGCCCTGAAAGCCATGAGATTTCTCATCTTGTGAGACCTAA 1680
 QY 1681 TCTCTGTAAGAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACATGTC 1740
 Db 1681 TCTCTGTAAGAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACATGTC 1740
 QY 1741 GCAGGACTCTAAACACAGACAGGCTCAAGTGTCTCTGAAACATATGAGTTGGAAT 1800
 Db 1741 GCAGGACTCTAAACACAGACAGGCTCAAGTGTCTCTGAAACATATGAGTTGGAAT 1800
 QY 1801 CACTGTTTGAACAACACACACTTACTTTTCTGTCTCTACCTGCTGATTTTCTCT 1860
 Db 1801 CACTGTTTGAACAACACACACTTACTTTTCTGTCTCTACCTGCTGATTTTCTCT 1860
 QY 1861 AGGAAATATATCTTTTACAGTAACAAATAAATAAATAAATAAATAAATAAATAAATAA 1920
 Db 1861 AGGAAATATATCTTTTACAGTAACAAATAAATAAATAAATAAATAAATAAATAAATAA 1920
 QY 1921 GAGTTACAGAAATGATTTACTTAAGGAGATTTACTCAGTAATTTGTTTAAAGTAATAAAA 1980
 Db 1921 GAGTTACAGAAATGATTTACTTAAGGAGATTTACTCAGTAATTTGTTTAAAGTAATAAAA 1980
 QY 1981 TTCAACAAACATTTGCTGGAATAGCTATATATGTCAGAGTCTGCAAGGATTTTACACTC 2040
 Db 1981 TTCAACAAACATTTGCTGGAATAGCTATATATGTCAGAGTCTGCAAGGATTTTACACTC 2040
 QY 2041 TGTAATTTGAATATTTATTTCTCAAAAATTCACATAGTAGAAGCTATCTGGGAAGCTAT 2100
 Db 2041 TGTAATTTGAATATTTATTTCTCAAAAATTTGCATAGTAGAAGCTATCTGGGAAGCTAT 2100
 QY 2101 TTTTTCAGTTTGAATTTCTAGCTTATCTTCTTCAAACTAATTTTATTTTGTCTGA 2160
 Db 2101 TTTTTCAGTTTGAATTTCTAGCTTATCTTCTTCAAACTAATTTTATTTTGTCTGA 2160
 QY 2161 GACTAATCTTATTTCTTCTTAAATGCAACCATTAATAACCTTAAATTTATTTTAAAC 2220
 Db 2161 GACTAATCTTATTTCTTCTTAAATGCAACCATTAATAACCTTAAATTTATTTTAAAC 2220
 QY 2221 ATACCTAAGAGTACATTTGTTACTCTTATATACCAAGCAATTTTAAAGTGCATTA 2280
 Db 2221 ATACCTAAGAGTACATTTGTTACTCTTATATACCAAGCAATTTTAAAGTGCATTA 2280
 QY 2281 CAATGATCACTAGCCCTCTTTTCCACAGAGGAGCTGAGAGATCGAGAAATATT 2340
 Db 2281 CAATGATCACTAGCCCTCTTTTCCACAGAGGAGCTGAGAGATCGAGAAATATT 2340
 QY 2341 TGTGACAAAAAATTTAAGCAATTTAGAAAACTT 2372
 Db 2341 TGTGACAAAAAATTTAAGCAATTTAGAAAACTT 2372

RESULT 4
 AAF92060
 ID AAF92060 standard; cdna; 2372 BP.
 XX AAF92060;
 XX AC
 XX XX
 DT 15-MAY-2001 (first entry)
 XX XX
 DE Human PRO263 cdna.

1321 CCTGTCTGGATCTATCTCTCTACCTCCAAAGCTTCCACGGCTTCTAGCTGGCTAT 1380
1381 GTCTTAATAATATCCCACTGGGAAAGAGTGTTCGAAAGTGCAAGGACTTAAACATC 1440
1381 GTCTTAATAATATCCCACTGGGAAAGAGTGTTCGAAAGTGCAAGGACTTAAACATC 1440
1441 TCATCAGTATCCAGTGTAAAGAGGCTCTCTGGCTGTCTGAGCTAGTGGTGAAGC 1500
1441 TCATCAGTATCCAGTGTAAAGAGGCTCTCTGGCTGTCTGAGCTAGTGGTGAAGC 1500
1501 CAAGGAGTCTACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
1501 CAAGGAGTCTACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
1561 GCTCTGAAGAGAGAAACACGTATCCCACTGACATGTCTTCTGAGCCGGTAAGAGCAAA 1620
1561 GCTCTGAAGAGAGAAACACGTATCCCACTGACATGTCTTCTGAGCCGGTAAGAGCAAA 1620
1621 AGAATGCGAGAAAGTTAGCCCTGAAAGCCATGGAGATTCCTAATCTTGAGACCTAA 1680
1621 AGAATGCGAGAAAGTTAGCCCTGAAAGCCATGGAGATTCCTAATCTTGAGACCTAA 1680
1681 TCTCTGTAAAGCTTAAATAAGAAATAGAAACAGGCTGAGGATACGACACTGTCTCA 1740
1681 TCTCTGTAAAGCTTAAATAAGAAATAGAAACAGGCTGAGGATACGACACTGTCTCA 1740
1741 GAGGAGCTGTAAACACAGACAGGCTCAAGTGTCTCTGAAACATTTGAGTTGGAAT 1800
1741 GAGGAGCTGTAAACACAGACAGGCTCAAGTGTCTCTGAAACATTTGAGTTGGAAT 1800
1801 CACTGTTTGAACACACACACTTACTTCTGCTCTACCACTGCTGATATTTCTCT 1860
1801 CACTGTTTGAACACACACACTTACTTCTGCTCTACCACTGCTGATATTTCTCT 1860
1861 AGGAATATATCTTTTCAAGTAAACAAAATAAAGAACTCTTATAAATTTCTATTTTATCT 1920
1861 AGGAATATATCTTTTCAAGTAAACAAAATAAAGAACTCTTATAAATTTCTATTTTATCT 1920
1921 GAGTTACAGAAATGATTAAGAAAGATTAATCAGTAAATTTGTTTAAAGTAATAAAA 1980
1921 GAGTTACAGAAATGATTAAGAAAGATTAATCAGTAAATTTGTTTAAAGTAATAAAA 1980
1981 TTCAAGACATTTGCTGATAGTACTATATCTCAAGTCTGTGCAAGGTATTACATC 2040
1981 TTCAAGACATTTGCTGATAGTACTATATCTCAAGTCTGTGCAAGGTATTACATC 2040
2041 TGTAATTTGAATATTTTCTTCAAGAAATTCACATAGTAGAAGCTATCTGGGAAGCTAT 2100
2041 TGTAATTTGAATATTTTCTTCAAGAAATTCACATAGTAGAAGCTATCTGGGAAGCTAT 2100
2101 TTTTTCAGTTTGAATTTCTAGTATCTTCTTCAAGTATCTTCCAACTAATTTTATTTTCTGA 2160
2101 TTTTTCAGTTTGAATTTCTAGTATCTTCTTCAAGTATCTTCCAACTAATTTTATTTTCTGA 2160
2161 GACTATCTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2220
2161 GACTATCTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2220
2221 ATACCTTAAGAGTACATTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2280
2221 ATACCTTAAGAGTACATTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2280
2281 CAAATGTATCCTAGGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2340
2281 CAAATGTATCCTAGGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2340
2341 TGTGACAAAAAATTAAGCAATTTAGAAACTT 2372
2341 TGTGACAAAAAATTAAGCAATTTAGAAACTT 2372

ABST74380

ID ABS74380 standard; cDNA; 2372 BP.

XX AC ABS74380;

XX XX 10-DEC-2002 (first entry)

XX DE Human cDNA encoding secreted/transmembrane protein PRO263.

XX XX Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.

XX OS Homo sapiens.

XX XX US2002119130-A1.

XX XX 29-AUG-2002.

XX XX 06-DEC-2001; 2001US-00006867.

XX XX 29-OCT-1997; 97US-0063435P.

XX XX 29-OCT-1997; 97US-0064215P.

XX XX 22-APR-1998; 98US-0082797P.

XX XX 29-APR-1998; 98US-0083495P.

XX XX 15-MAY-1998; 98US-0085579P.

XX XX 02-JUN-1998; 98US-0087759P.

XX XX 04-JUN-1998; 98US-0088021P.

XX XX 04-JUN-1998; 98US-0088030P.

XX XX 10-JUN-1998; 98US-0088734P.

XX XX 10-JUN-1998; 98US-0088740P.

XX XX 10-JUN-1998; 98US-0088811P.

XX XX 10-JUN-1998; 98US-0088824P.

XX XX 10-JUN-1998; 98US-0088825P.

XX XX 12-JUN-1998; 98US-0088963P.

XX XX 16-JUN-1998; 98US-0089105P.

XX XX 16-JUN-1998; 98US-0089514P.

XX XX 17-JUN-1998; 98US-0089653P.

XX XX 19-JUN-1998; 98US-0089952P.

XX XX 22-JUN-1998; 98US-0090246P.

XX XX 24-JUN-1998; 98US-0090444P.

XX XX 25-JUN-1998; 98US-0090688P.

XX XX 25-JUN-1998; 98US-0090896P.

XX XX 26-JUN-1998; 98US-0090862P.

XX XX 02-JUL-1998; 98US-0091628P.

XX XX 10-AUG-1998; 98US-0096012P.

XX XX 17-AUG-1998; 98US-0096757P.

XX XX 18-AUG-1998; 98US-0096949P.

XX XX 18-AUG-1998; 98US-0096959P.

XX XX 26-AUG-1998; 98US-0097954P.

XX XX 26-AUG-1998; 98US-0097971P.

XX XX 01-SEP-1998; 98US-0097979P.

XX XX 01-SEP-1998; 98US-0098749P.

XX XX 10-SEP-1998; 98US-0099741P.

XX XX 10-SEP-1998; 98US-0099763P.

XX XX 10-SEP-1998; 98US-0099792P.

XX XX 10-SEP-1998; 98US-0099812P.

XX XX 16-SEP-1998; 98US-0099815P.

XX XX 16-SEP-1998; 98US-0100627P.

XX XX 16-SEP-1998; 98US-0100662P.

XX XX 16-SEP-1998; 98US-0100683P.

XX XX 17-SEP-1998; 98US-0100684P.

XX XX 17-SEP-1998; 98US-0100930P.

XX XX 22-SEP-1998; 98US-0101279P.

XX XX 23-SEP-1998; 98US-0101475P.

XX XX 24-SEP-1998; 98US-0101738P.

XX XX 24-SEP-1998; 98US-0101743P.

XX XX 24-SEP-1998; 98US-0101916P.

XX XX 30-SEP-1998; 98US-0102570P.

XX XX 06-OCT-1998; 98US-0103449P.

XX XX 08-MAR-1999; 99WO-US005028.

PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 28-FEB-2001; 2001WO-US004956.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Gramaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2002-731348/79.
DR P-PSDB; ABG95853.
XX
PT New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
PS Claim 2; Fig 5; 399pp; English.
XX
XX The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as A/E, B/F, B/G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation

CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
CC invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCAGGGAATCCGGATGTCGCTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
DB 1 AGCAGGGAATCCGGATGTCGCTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
QY 61 GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
DB 61 GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
QY 121 CATCTGAGTGTTCCTTCCCTGGCTCTGAAGGGGTAGGCAGATGCCAGTGTTCAGCCTG 180
DB 121 CATCTGAGTGTTCCTTCCCTGGCTCTGAAGGGGTAGGCAGATGCCAGTGTTCAGCCTG 180
QY 181 GTGTGCTTCTCAGTTCATCTGCACACAGGCTCCTGTGTCAGAGGCTCTTTGGGTGCA 240
DB 181 GTGTGCTTCTCAGTTCATCTGCACACAGGCTCCTGTGTCAGAGGCTCTTTGGGTGCA 240
QY 241 GAAGAGCTTTCCATCCAGGTGTCATGAGAAATTATGGGATCACCTTTGTGAGCAAAAAG 300
DB 241 GAAGAGCTTTCCATCCAGGTGTCATGAGAAATTATGGGATCACCTTTGTGAGCAAAAAG 300
QY 301 GCGAACCCAGAGCTGAATTTACAGAGCTTAAGAGGCTCTAGGCTCTGGGACTAAGT 360
DB 301 GCGAACCCAGAGCTGAATTTACAGAGCTTAAGAGGCTCTAGGCTCTGGGACTAAGT 360
QY 361 TTGCGCGGCAAGGACCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTGAACTTGACGCTAT 420
DB 361 TTGCGCGGCAAGGACCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTGAACTTGACGCTAT 420
QY 421 GGCTGGGTGGAGATGGAATTCGCTGATCTCTAGGATTTAGCCCAACCCCAAGTGGG 480
DB 421 GGCTGGGTGGAGATGGAATTCGCTGATCTCTAGGATTTAGCCCAACCCCAAGTGGG 480
QY 481 AAAAATGGGTGGGTGCTCTGATTTGAGAGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
DB 481 AAAAATGGGTGGGTGCTCTGATTTGAGAGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
QY 541 TGTTCACAACTCATCTGATACCTTGCACTAACTCGTGCAATTCAGAAATATCACCAACAAA 600
DB 541 TGTTCACAACTCATCTGATACCTTGCACTAACTCGTGCAATTCAGAAATATCACCAACAAA 600
QY 601 GATCCCATATTCAACACTCAAACTGCAACAAACAAACAGAAATTTATTGTGAGTACAGT 660
DB 601 GATCCCATATTCAACACTCAAACTGCAACAAACAAACAGAAATTTATTGTGAGTACAGT 660
QY 661 ACCTACTCGGTGGATCCCTTACTCTACATACCTGCGCCTACTACTCTCTCTCTGCT 720
DB 661 ACCTACTCGGTGGATCCCTTACTCTACATACCTGCGCCTACTACTCTCTCTCTGCT 720
QY 721 CCAGCTTCCACTTCTATTCCAGGAGAAAAAATTTGATTTGTGTCACAGAAATTTTATG 780
DB 721 CCAGCTTCCACTTCTATTCCAGGAGAAAAAATTTGATTTGTGTCACAGAAATTTTATG 780
QY 781 GAAACTAGCAACATGCTTACAGAACTGAACCATTTGTTGAAAAATAAGACAGCATTCAG 840
DB 781 GAAACTAGCAACATGCTTACAGAACTGAACCATTTGTTGAAAAATAAGACAGCATTCAG 840
QY 841 AATGAGCTGTGGTGTGGAGGTGTCGCCAGGCTCTGAGTGTGCTCTCTCTCTCTC 900
DB 841 AATGAGCTGTGGTGTGGAGGTGTCGCCAGGCTCTGAGTGTGCTCTCTCTCTCTC 900

Db 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCAAGGCTCTGCTAGTGTCTCTCTCTTC 900
QY 901 TTTCGCTCTGAGCTGCTGCTTGGATTTTGGTATCTCAAAAGGTATGTGAAGCCCTTCCT 960
Db 901 TTTCGCTCTGAGCTGCTGCTTGGATTTTGGTATCTCAAAAGGTATGTGAAGCCCTTCCT 960
QY 961 TTTTCAACAAGAAATCAGCAGGAAGAAATGATCGAAAACCAAGTAGTAAAGGAGGAGAAG 1020
Db 961 TTTTCAACAAGAAATCAGCAGGAAGAAATGATCGAAAACCAAGTAGTAAAGGAGGAGAAG 1020
QY 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACCTGATATAAAACCCAGAGAGTCC 1080
Db 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACCTGATATAAAACCCAGAGAGTCC 1080
QY 1081 AAGAGTCCAAAGCAAAATACCGTCCGATGCTGGAAGTGAAGTTTGAATGAGACAGAAA 1140
Db 1081 AAGAGTCCAAAGCAAAATACCGTCCGATGCTGGAAGTGAAGTTTGAATGAGACAGAAA 1140
QY 1141 TGAGGAGACACACTGAGGCTGGTTCTTTCATGCTCTTACCCCTGCCAGCTGGGGAA 1200
Db 1141 TGAGGAGACACACTGAGGCTGGTTCTTTCATGCTCTTACCCCTGCCAGCTGGGGAA 1200
QY 1201 ATCAAAAGGCCAAAGAAACCAAGAGTCCACCCCTGGTTCCTAACTTGAATCAGC 1260
Db 1201 ATCAAAAGGCCAAAGAAACCAAGAGTCCACCCCTGGTTCCTAACTTGAATCAGC 1260
QY 1261 TCAGGAGTCCATGGACTGAGTGCACCAAGAGAAATGCCCTTCTCTTATTGTAAC 1320
Db 1261 TCAGGAGTCCATGGACTGAGTGCACCAAGAGAAATGCCCTTCTCTTATTGTAAC 1320
QY 1321 CCTGTCTGATCT 1380
Db 1321 CCTGTCTGATCT 1380
QY 1381 GTCTTAATATATCCCACTGGGAGAAAGAGTGTTCGAAAGTGCAGGACCTTAAACATC 1440
Db 1381 GTCTTAATATATCCCACTGGGAGAAAGAGTGTTCGAAAGTGCAGGACCTTAAACATC 1440
QY 1441 TCATCAGTATCCAGTGTAAAGAGGCTCTGCTGCTGTCTGAGGCTAGTGGTGTGAAGC 1500
Db 1441 TCATCAGTATCCAGTGTAAAGAGGCTCTGCTGCTGTCTGAGGCTAGTGGTGTGAAGC 1500
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCCAGCTCAGACCCCTTCTTCA 1560
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCCAGCTCAGACCCCTTCTTCA 1560
QY 1561 GCTCTGAAGAGAAAACAGTATCCCACTGACATGCTCTCTGAGCCGGTAAAGACAAA 1620
Db 1561 GCTCTGAAGAGAAAACAGTATCCCACTGACATGCTCTCTGAGCCGGTAAAGACAAA 1620
QY 1621 AGAATGCGAGAAAGTTTACGCCCTGAAAGCCATGGAGTCTCTATAACTTTGAGACCTAA 1680
Db 1621 AGAATGCGAGAAAGTTTACGCCCTGAAAGCCATGGAGTCTCTATAACTTTGAGACCTAA 1680
QY 1681 TCTCTGTAAGCTTAAATAAAGAAATAGAACCAAGGCTGAGGATACGACATGCTCA 1740
Db 1681 TCTCTGTAAGCTTAAATAAAGAAATAGAACCAAGGCTGAGGATACGACATGCTCA 1740
QY 1741 GCAGGAGCTGTAACACAGACAGGGTCAAGTGTCTCTCTGACACATTTGAGTGGAAAT 1800
Db 1741 GCAGGAGCTGTAACACAGACAGGGTCAAGTGTCTCTCTGACACATTTGAGTGGAAAT 1800
QY 1801 CACTGTTTGAACACACACACTTACTTTTCTGCTCTCTACCACTGCTGATTTTCTCT 1860
Db 1801 CACTGTTTGAACACACACACTTACTTTTCTGCTCTCTACCACTGCTGATTTTCTCT 1860
QY 1861 AGGAATATATCTTTTACAGTAAACAAAATATAAAATCTCTTATAAAATTTCTTTTATCT 1920
Db 1861 AGGAATATATCTTTTACAGTAAACAAAATATAAAATCTCTTATAAAATTTCTTTTATCT 1920
QY 1921 GAGTTACAGAAATGATTTACTAAGGAAGTACTCAGTAAATTTGTTTTAAAGTAATAAAA 1980
Db 1921 GAGTTACAGAAATGATTTACTAAGGAAGTACTCAGTAAATTTGTTTTAAAGTAATAAAA 1980

QY 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGCTGCAAGGTATTACACTC 2040
Db 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGCTGCAAGGTATTACACTC 2040
QY 2041 TGTAAATTTGAATATTATTCTCTCAAAAATTTGCATAGTAGAACGCTATCTGGGAAGCTAT 2100
Db 2041 TGTAAATTTGAATATTATTCTCTCAAAAATTTGCATAGTAGAACGCTATCTGGGAAGCTAT 2100
QY 2101 TTTTTCAGTTTGTGATTTTCTAGCTTATCTTCTCAAACTAATTTTATTTTGTCTGA 2160
Db 2101 TTTTTCAGTTTGTGATTTTCTAGCTTATCTTCTCAAACTAATTTTATTTTGTCTGA 2160
QY 2161 GACTAATCTTTTCAATTTTCTTAATATGGAACCAATATAA CTTTAATTTATTATTAAC 2220
Db 2161 GACTAATCTTTTCAATTTTCTTAATATGGAACCAATATAA CTTTAATTTATTATTAAC 2220
QY 2221 ATACCTAAGAAGTACATTTTACCTCTATATACCAAGACATTTTAAAGTGCCATTAA 2280
Db 2221 ATACCTAAGAAGTACATTTTACCTCTATATACCAAGACATTTTAAAGTGCCATTAA 2280
QY 2281 CAAATGTATCACTAGCCCTCTTTTCCAAAGAGAGGACTGAGAGATGCAGAAATATT 2340
Db 2281 CAAATGTATCACTAGCCCTCTTTTCCAAAGAGAGGACTGAGAGATGCAGAAATATT 2340
QY 2341 TGTGACAAAAAATTAAGCATTTAGAAAACCTT 2372
Db 2341 TGTGACAAAAAATTAAGCATTTAGAAAACCTT 2372

RESULT 6
ABL88087
ID ABL88087 standard; cdna; 2372 BP.
XX ABL88087;
AC AC
XX XX
XX XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO263 cDNA sequence SEQ ID NO:31.
XX
KW Human; angiogenesis; cardiac; dilatant; cytostatic; antiangiogenic; hypotensive;
vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
gene therapy; cardiovascular disorder; endothelial disorder; cancer;
angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
age-related macular degeneration; arterial restenosis; angina;
rheumatoid arthritis; myocardial infarction; thrombophlebitis;
lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
wound healing; chromosome mapping; gene mapping; gene; ss.
OS Homo sapiens.
XX
XX
FN WO200200690-A2.
XX
XX
PD 03-JAN-2002.
XX
XX
PF 20-JUN-2001; 2001WO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX (GETH) GENENTECH INC.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-090516/12.
DR P-PSDB; ABB84832.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 2; Fig 31; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCAGGAAATCCGATCTCTCGTTATACAGTGAGCAGTGAGTGAGCCCTCAACATA 60
DB 1 AGCAGGAAATCCGATCTCTCGTTATACAGTGAGCAGTGAGTGAGCCCTCAACATA 60
QY 61 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC 120
DB 61 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC 120
QY 121 CATCTGAGTGTTTCCCTGCTGAGGGGTAGGACGATGGCCAGGTGCTTCAGCCTG 180
DB 121 CATCTGAGTGTTTCCCTGCTGAGGGGTAGGACGATGGCCAGGTGCTTCAGCCTG 180
QY 181 GTGTGCTTCTCATTCCATCTGGACACGAGGCTCTGGTCCAGGCTCTTTTGGTGCA 240
DB 181 GTGTGCTTCTCATTCCATCTGGACACGAGGCTCTGGTCCAGGCTCTTTTGGTGCA 240
QY 241 GAAGAGCTTTCCATCCAGGTGTATGAGAAATTTATGGGATCACCCTTGTGAGCAAAAG 300

241 GAAGAGCTTTCCATCCAGGTGTATGAGAAATTTATGGGATCACCCTTGTGAGCAAAAG 300
QY 301 GCGAACAGCAGCTGAATTTTACAGAAAGTAAAGAGGCTCTAGGCTCTCTGGACTAAAGT 360
DB 301 GCGAACAGCAGCAGCTGAATTTTACAGAAAGTAAAGAGGCTCTAGGCTCTCTGGACTAAAGT 360
QY 361 TTGGCCGCGCAGGACCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTTGAACCTTGACGCTAT 420
DB 361 TTGGCCGCGCAGGACCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTTGAACCTTGACGCTAT 420
QY 421 GGCTGGGTTGAGATGAGATTCGTGCTCATCTCTAGGATAGCCCAACCCCAAGTGTGGG 480
DB 421 GGCTGGGTTGAGATGAGATTCGTGCTCATCTCTAGGATAGCCCAACCCCAAGTGTGGG 480
QY 481 AAAAATGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTAT 540
DB 481 AAAAATGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTAT 540
QY 541 TGTACAACTCATCTGATACCTTGGACTAACTCGTGCATTCAGAAATTTATCACCACCAA 600
DB 541 TGTACAACTCATCTGATACCTTGGACTAACTCGTGCATTCAGAAATTTATCACCACCAA 600
QY 601 GATCCATATTTCAACACTCAAACTGCAACACCAACAGAAATTTATTTGTGAGTACAGT 660
DB 601 GATCCATATTTCAACACTCAAACTGCAACACCAACAGAAATTTATTTGTGAGTACAGT 660
QY 661 ACCTACTCGGTGGGATCCCTTACTCTACAATACCTGCTCCCTTACTTACTTCTCTCTGCT 720
DB 661 ACCTACTCGGTGGGATCCCTTACTCTACAATACCTGCTCCCTTACTTACTTCTCTCTGCT 720
QY 721 CCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTTGATTTGTGTGTCACAGAAATTTATG 780
DB 721 CCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTTGATTTGTGTGTCACAGAAATTTATG 780
QY 781 GAACTAGACCATGTCTACAGAACTGAACCAATTTGTGAAAAATTAAGCAGCATTCAG 840
DB 781 GAACTAGACCATGTCTACAGAACTGAACCAATTTGTGAAAAATTAAGCAGCATTCAG 840
QY 841 AATGAAGCTGTGGTGGGAGGTGTCGCCAGGCTCTGCTAGTGTCTTCTCTCTCTCTCTC 900
DB 841 AATGAAGCTGTGGTGGGAGGTGTCGCCAGGCTCTGCTAGTGTCTTCTCTCTCTCTCTC 900
QY 901 TTTGTGTCTGAGCTGTGCTTTGGATTTTGTCTATGTCAAAAGTATGTGAAGGCTTCCCT 960
DB 901 TTTGTGTCTGAGCTGTGCTTTGGATTTTGTCTATGTCAAAAGTATGTGAAGGCTTCCCT 960
QY 961 TTTCAAAACAGAAATCAGCAGAAAGAAATGATCGAAACCAAGTATGAAGGAGGAGAG 1020
DB 961 TTTCAAAACAGAAATCAGCAGAAAGAAATGATCGAAACCAAGTATGAAGGAGGAGAG 1020
QY 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAATCTGATAAAATCCAGAGAGTCC 1080
DB 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAATCTGATAAAATCCAGAGAGTCC 1080
QY 1081 AAGAGTCCAAAGCAAACTACCGTGGATGCTCCCTGGAAGTGAAGTTAGATGAGACAGAAA 1140
DB 1081 AAGAGTCCAAAGCAAACTACCGTGGATGCTCCCTGGAAGTGAAGTTAGATGAGACAGAAA 1140
QY 1141 TGAGAGACACACTGAGGCTGGTTTCTTCTGATGCTCTTACCTGCCCCAGCTGGGAA 1200
DB 1141 TGAGAGACACACTGAGGCTGGTTTCTTCTGATGCTCTTACCTGCCCCAGCTGGGAA 1200
QY 1201 ATCAAAAGGGCCAAAGAAACCAAGAAAGTCCACCTTGGTTCCTTAATGGAATCAGC 1260
DB 1201 ATCAAAAGGGCCAAAGAAACCAAGAAAGTCCACCTTGGTTCCTTAATGGAATCAGC 1260
QY 1261 TCAGGACTGCCATTTGGAATGATGAGTGCACCAAGAGAAATGCTCTCTTATTGTAAC 1320
DB 1261 TCAGGACTGCCATTTGGAATGATGAGTGCACCAAGAGAAATGCTCTCTTATTGTAAC 1320
QY 1321 CTTGTCTGGATCCTATCTCTCTTACCTCCAAAGCTTCCACGGCTTTCTAGCTGGCTAT 1380
DB 1321 CTTGTCTGGATCCTATCTCTCTTACCTCCAAAGCTTCCACGGCTTTCTAGCTGGCTAT 1380

Db 1321 CCTGTCGTGATCCTATCTCTCTCCCTCCAAAGCTTCCACGGCTTTCTAGCCCTGGCTAT 1380
 QY 1381 GTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGGCAAGTGAAGACCTTAAACATC 1440
 Db 1381 GTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGGCAAGTGAAGACCTTAAACATC 1440
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 Db 1441 TCATCAGTATCCAGTGTGTAAGAGGCTCTCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500
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 Db 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGACAGCTCAGACCCCTTCTTCA 1560
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 Db 1561 GCTCTGAAGAGAGAAACAGCTATCCACCTGACATGCTCTTCTGAGCCCGGTAAAGCAAAA 1620
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 Db 1621 AGAATGGCAGAAAGTTAGTCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
 QY 1681 TCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA 1740
 Db 1681 TCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA 1740
 QY 1741 GCAGGAGTCTAAACACAGACAGGCTCAAGGTGTTTCTCTGACACATTTGAGTTGGAAT 1800
 Db 1741 GCAGGAGTCTAAACACAGACAGGCTCAAGGTGTTTCTCTGACACATTTGAGTTGGAAT 1800
 QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860
 Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860
 QY 1861 AGGAAATATCTTTTCAAGTAAACAAATAAAGAACTCTTATAAACTTTATTTTATCT 1920
 Db 1861 AGGAAATATCTTTTCAAGTAAACAAATAAAGAACTCTTATAAACTTTATTTTATCT 1920
 QY 1921 GAGTTACAGAAATGATTAAGGAATTAAGTACTGAGTAAATTTGTTTAAAGTAAATAAA 1980
 Db 1921 GAGTTACAGAAATGATTAAGGAATTAAGTACTGAGTAAATTTGTTTAAAGTAAATAAA 1980
 QY 1981 TTCAACAAACATTTGCTGATAGTACTATATGTCAAGTCTGTGCAAGGTATTAACATC 2040
 Db 1981 TTCAACAAACATTTGCTGATAGTACTATATGTCAAGTCTGTGCAAGGTATTAACATC 2040
 QY 2041 TGTAATTTGAATATTTCTTCAAAAATTCACATAGTAGAAGCTATCTGGGAAGCTAT 2100
 Db 2041 TGTAATTTGAATATTTCTTCAAAAATTCACATAGTAGAAGCTATCTGGGAAGCTAT 2100
 QY 2101 TTTTTCAGTTTGTATATTTCTAGCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2160
 Db 2101 TTTTTCAGTTTGTATATTTCTAGCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2160
 QY 2161 GACTATCTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2220
 Db 2161 GACTATCTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2220
 QY 2221 ATACCTAAGAGTACATTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2280
 Db 2221 ATACCTAAGAGTACATTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2280
 QY 2281 CAAATGTATCAGTACGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2340
 Db 2281 CAAATGTATCAGTACGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2340
 QY 2341 TGTGACAAAAAATTAAGACATTTAGAAAACTT 2372
 Db 2341 TGTGACAAAAAATTAAGACATTTAGAAAACTT 2372

ID ABL95576 standard; cDNA; 2372 BP.
 XX ABL95576;
 AC 19-JUL-2002 (first entry)
 XX Human angiogenesis related cDNA PRO263 SEQ ID NO: 31.
 DE Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiant; cytosstatic; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic; gene; ss.
 XX Homo sapiens.
 OS WO200208284-A2.
 XX 31-JAN-2002.
 PD 09-JUL-2001; 2001WO-US021735.
 PF 20-JUL-2000; 2000US-0219556P.
 XX 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 01-MAR-2001; 2001WO-US006520.
 PR 03-MAR-2001; 2001WO-US006566.
 PR 14-MAR-2001; 2001US-00802706.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-0086028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 XX (GETH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODO) GODOWSKI P J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANJ) PAN J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; 720
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF; 720
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W; 720
XX WPI; 2002-171999/22. 780
DR P-PSDB; ABB95438. 780
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides, 840
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial 840
PT infarction), endothelial or angiogenic disorders in a mammal. 840
XX Claim 1; Fig 31; 567pp; English. 840
XX The present invention provides the protein and coding sequences of human 900
CC PRO proteins. These are useful for treating or diagnosing a 900
CC cardiovascular, endothelial or angiogenic disorder, including a 900
CC hypertrophy, trauma, cancer, age-related macular degeneration, 900
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, 900
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour 900
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound 900
CC healing. The present sequence is a coding sequence of the invention 900
XX Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other; 900
SQ Query Match 100.0%; Score 2372; DB 6; Length 2372; 900
Best Local Similarity 100.0%; Pred. No. 0; 900
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 900
QY 1 AGCAGGGAAATCCGGATGCTCGGTATGAAAGTGGAGCAGTGGAGCTCAACATA 60
DB 1 AGCAGGGAAATCCGGATGCTCGGTATGAAAGTGGAGCAGTGGAGCTCAACATA 60
QY 61 GTTCCAGAACTCCATCCGACTAGTATTGAGCATCTGCTCTCATATCACCAGTGC 120
DB 61 GTTCCAGAACTCCATCCGACTAGTATTGAGCATCTGCTCTCATATCACCAGTGC 120
QY 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGTGGACGATGGCGGCTTTCAGCCTG 180
DB 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGTGGACGATGGCGGCTTTCAGCCTG 180
QY 181 GTGTGCTTCTCAGTCCATCGGACGAGGCTCTGGTCCAAAGGCTTTGGGTGCA 240
DB 181 GTGTGCTTCTCAGTCCATCGGACGAGGCTCTGGTCCAAAGGCTTTGGGTGCA 240
QY 241 GAAGAGCTTTCCATCCAGGTGTCAGAGAAATATGGGATCACCTTTGAGCAAAAG 300
DB 241 GAAGAGCTTTCCATCCAGGTGTCAGAGAAATATGGGATCACCTTTGAGCAAAAG 300
QY 301 GCGAACCAAGCAGTGAATTTACAGAACTAAGAGGCTGTAGGCTGTGGGACTAAGT 360
DB 301 GCGAACCAAGCAGTGAATTTACAGAACTAAGAGGCTGTAGGCTGTGGGACTAAGT 360
QY 361 TTGGCCGCAAGGACCAAGTTGAACAGCCTTGAAGCTAGCTTTGAACCTTGAGCTAT 420
DB 361 TTGGCCGCAAGGACCAAGTTGAACAGCCTTGAAGCTAGCTTTGAACCTTGAGCTAT 420
QY 421 GGCTGGGTGGAGATGGATGCTGCTCATCTAGATTAGCCCAACCCCAAGTGTGG 480
DB 421 GGCTGGGTGGAGATGGATGCTGCTCATCTAGATTAGCCCAACCCCAAGTGTGG 480
QY 481 AAAAATGGGTGGGTGCTGCTGATTTGGAAGGTTCAGTGAGCCGACAGTTTGCAGCTAT 540
DB 481 AAAAATGGGTGGGTGCTGCTGATTTGGAAGGTTCAGTGAGCCGACAGTTTGCAGCTAT 540
QY 541 TGTTCACATCATCTGACTACTTGGATCTAACTGCTGCTGATTCAGAAATATCAACCAAA 600
DB 541 TGTTCACATCATCTGACTACTTGGATCTAACTGCTGCTGATTCAGAAATATCAACCAAA 600
QY 601 GATCCCATATCAACACTCAAACTGCAACACAAACACAGATTTATTGTGAGTGCAGT 660
DB 601 GATCCCATATCAACACTCAAACTGCAACACAAACACAGATTTATTGTGAGTGCAGT 660

QY 661 ACCTACTCGGTGGCATCCCTTACTTACAACTACCTGCCCTTACTTACTTCTCTCTGCT 720
DB 661 ACCTACTCGGTGGCATCCCTTACTTACAACTACCTGCCCTTACTTACTTCTCTCTGCT 720
QY 721 CCAGCTTCCACTTCTTATTCACGGAGAAAAAATGATTTGTGTCACAGAGTTTATG 780
DB 721 CCAGCTTCCACTTCTTATTCACGGAGAAAAAATGATTTGTGTCACAGAGTTTATG 780
QY 781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAGCAGCATTCAG 840
DB 781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAGCAGCATTCAG 840
QY 841 AATGAAGCTGCTGGTGTGGAGGTTCCTCCACGGCTCTGCTAGTGTCTCTCTCTTC 900
DB 841 AATGAAGCTGCTGGTGTGGAGGTTCCTCCACGGCTCTGCTAGTGTCTCTCTCTTC 900
QY 901 TTTGGTGTGCTGAGCTGCTTGGATTTTGTATGTCACAAAGGTATGTGAAGGCTTCCCT 960
DB 901 TTTGGTGTGCTGAGCTGCTTGGATTTTGTATGTCACAAAGGTATGTGAAGGCTTCCCT 960
QY 961 TTTTCAAAACAAGAAATCAGCAGAGGAAATGATCGAAACCAAAGTAGTAAAGAGGAGAAG 1020
DB 961 TTTTCAAAACAAGAAATCAGCAGAGGAAATGATCGAAACCAAAGTAGTAAAGAGGAGAAG 1020
QY 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAATACTGATAAAACCCAGAGAGTCC 1080
DB 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAATACTGATAAAACCCAGAGAGTCC 1080
QY 1081 AAGAGTCCAAAGCAAACTACCGTGGATGCTGGAAGTGAAGTTAGATGAGCAGAGAA 1140
DB 1081 AAGAGTCCAAAGCAAACTACCGTGGATGCTGGAAGTGAAGTTAGATGAGCAGAGAA 1140
QY 1141 TGAGGAGACACACCTGAGGCTGTTCTTTTCATGCTCTTACCTGCTCCCTGAGCTGGGAA 1200
DB 1141 TGAGGAGACACACCTGAGGCTGTTCTTTTCATGCTCTTACCTGCTCCCTGAGCTGGGAA 1200
QY 1201 ATCAAAAGGGCCAAAGAAACCAAGAGAAAGTCCAACCTTGGTTCCTAACTGGAATCAGC 1260
DB 1201 ATCAAAAGGGCCAAAGAAACCAAGAGAAAGTCCAACCTTGGTTCCTAACTGGAATCAGC 1260
QY 1261 TCAGGACTGCTTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCTTATGTATAC 1320
DB 1261 TCAGGACTGCTTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCTTATGTATAC 1320
QY 1321 CCTGCTGGATCT 1380
DB 1321 CCTGCTGGATCT 1380
QY 1381 GTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGCAAGTGCAGGACCTTAAACATC 1440
DB 1381 GTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGCAAGTGCAGGACCTTAAACATC 1440
QY 1441 TCATCAGTATCCAGTGGTAAAAGGCTCTCTGGCTGTCTGAGGCTAGTGGTTCGAAAGC 1500
DB 1441 TCATCAGTATCCAGTGGTAAAAGGCTCTCTGGCTGTCTGAGGCTAGTGGTTCGAAAGC 1500
QY 1501 CAAGAGGTCACTGAGACCAAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 1560
DB 1501 CAAGAGGTCACTGAGACCAAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 1560
QY 1561 GCTCTGAAAGAGAAACAGGTATCCACCTGACATGCTCTCTCTCTCTCTCTCTCTCTCTCT 1620
DB 1561 GCTCTGAAAGAGAAACAGGTATCCACCTGACATGCTCTCTCTCTCTCTCTCTCTCTCTCT 1620
QY 1621 AGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCCTATACTTCTGAGACCTTAA 1680
DB 1621 AGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCCTATACTTCTGAGACCTTAA 1680
QY 1681 TCTCTGTAAGCTAAAATAAAGAAATAGAAACCAAGGCTGAGGATACGACAGTACCTGTCA 1740
DB 1681 TCTCTGTAAGCTAAAATAAAGAAATAGAAACCAAGGCTGAGGATACGACAGTACCTGTCA 1740
QY 1741 GCAGGGAATGTAAACACAGACAGGCTCAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800

Db	1741	GCAGGACTGTAACACACAGACAGGGTCAAGTGTCTCTCTGACACATTTGAGTTGAAT	1800	PR	17-SEP-1997;	97US-0059119P.
QY	1801	CACGTGTTAGAACACACACACCTTACTTTTCTGTGTCCTACCACTGCTGATATTTCTCT	1860	PR	17-SEP-1997;	97US-0059121P.
Db	1801	CACGTGTTAGAACACACACACCTTACTTTTCTGTGTCCTACCACTGCTGATATTTCTCT	1860	PR	17-SEP-1997;	97US-0059122P.
QY	1861	AGGAATATATCTTTTACAGTAAACAAAATAAAACCTTATAAATTTCTATTTTATCT	1920	PR	18-SEP-1997;	97US-0059263P.
Db	1861	AGGAATATATCTTTTACAGTAAACAAAATAAAACCTTATAAATTTCTATTTTATCT	1920	PR	18-SEP-1997;	97US-0059266P.
QY	1921	GAGTTACAGAAATGATTACTAAGGAAGATTAATCAGTAAATTTGTTTAAAAAGTAATAAAA	1980	PR	15-OCT-1997;	97US-0062125P.
Db	1921	GAGTTACAGAAATGATTACTAAGGAAGATTAATCAGTAAATTTGTTTAAAAAGTAATAAAA	1980	PR	15-OCT-1997;	97US-0062285P.
QY	1981	TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGCGAAGGTATTACACTC	2040	PR	17-OCT-1997;	97US-0062287P.
Db	1981	TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGCGAAGGTATTACACTC	2040	PR	17-OCT-1997;	97US-0062486P.
QY	2041	TGTAATTTGAATATTTATTCCTCAAAAAATTCACATAGTAGAAGCTATCTGGGAAGCTAT	2100	PR	21-OCT-1997;	97US-0063486P.
Db	2041	TGTAATTTGAATATTTATTCCTCAAAAAATTCACATAGTAGAAGCTATCTGGGAAGCTAT	2100	PR	24-OCT-1997;	97US-0063486P.
QY	2101	TTTTTTCAGTTTGAATTTCTAGCTTATCTTCTCAAAACTAATTTTATTTTGTCTGA	2160	PR	24-OCT-1997;	97US-0063121P.
Db	2101	TTTTTTCAGTTTGAATTTCTAGCTTATCTTCTCAAAACTAATTTTATTTTGTCTGA	2160	PR	24-OCT-1997;	97US-0063127P.
QY	2161	GACTAATCTTATTTCTTAATTTGGAACCATTAATTAATTTATTTATTTATTAAC	2220	PR	24-OCT-1997;	97US-0063128P.
Db	2161	GACTAATCTTATTTCTTAATTTGGAACCATTAATTAATTTATTTATTTATTAAC	2220	PR	24-OCT-1997;	97US-0063327P.
QY	2221	ATACCTAAGAGTACATTTGTTTACTCTATATACCAAGACATTTTAAAGTGCCATTAA	2280	PR	27-OCT-1997;	97US-0063329P.
Db	2221	ATACCTAAGAGTACATTTGTTTACTCTATATACCAAGACATTTTAAAGTGCCATTAA	2280	PR	28-OCT-1997;	97US-0063341P.
QY	2281	CAATGTTATCCTAGCCCTCTTTTCCAAAGAGGAGTCTGAGAGATGCAGAAATATT	2340	PR	28-OCT-1997;	97US-0063549P.
Db	2281	CAATGTTATCCTAGCCCTCTTTTCCAAAGAGGAGTCTGAGAGATGCAGAAATATT	2340	PR	28-OCT-1997;	97US-0063550P.
QY	2341	TGTGACAAAAAATTAAGCAATTTAGAAAACTT	2372	PR	29-OCT-1997;	97US-0063564P.
Db	2341	TGTGACAAAAAATTAAGCAATTTAGAAAACTT	2372	PR	29-OCT-1997;	97US-0063435P.
RESULT 8						
ACAS9060						
ID	ACAS9060	standard; cdna; 2372 BP.				
AC	ACAS9060;					
XX						
DT	16-JUN-2003	(first entry)				
XX						
DE	Human PRO polynucleotide #36.					
KW	Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;					
KW	pathological disorder; cardiac insufficiency disorder; protein secretion;					
KW	pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;					
KW	skin disease; keratinocyte differentiation; epithelial cancer; tumor;					
KW	lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;					
KW	cytostatic; cardiac; endocrine; antidiabetic; gastrointestinal;					
KW	antulcer; dermatological; vulnary.					
OS	Homo sapiens.					
XX						
FN	US2002146709-A1.					
XX						
PD	10-OCT-2002.					
XX						
PF	18-JUL-2001; 2001US-00909088.					
XX						
PR	17-SEP-1997; 97US-0059113P.					
PR	17-SEP-1997; 97US-0059115P.					
PR	17-SEP-1997; 97US-0059117P.					

PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Macher JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 XX Williams PM, Wood WI;
 DR WPI; 2003-328338/31.
 DR P-PSDB; ABU71625.
 XX Isolated nucleic acid useful for e.g., treating pathological disorders
 PT encodes a secreted or transmembrane protein.
 XX Claim 2; Fig 73; 473pp; English.
 XX The invention relates to human PRO polypeptides (secreted or
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC PRO polypeptides and polynucleotides can be used in treating pathological
 CC disorders and tumours, in therapeutic treatment of cardiac insufficiency
 CC disorders and in therapeutic treatment of disorders involving protein
 CC secretion by the pancreas, including diabetes. They can also be used in
 CC treating disorders associated with the preservation and maintenance of
 CC gastrointestinal mucosa and the repair of acute and chronic mucosal
 CC lesions, and skin diseases associated with abnormal keratinocyte
 CC differentiation (e.g., psoriasis, epithelial cancers such as lung
 CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).
 CC The sequences can be used as molecular markers for protein
 CC electrophoresis purposes and can be utilised in protein-protein binding
 CC assays, biochemical screening assays, immunoassays and cell-based assays.
 CC This sequence represents a human PRO polynucleotide of the invention
 XX
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2372; DB 7; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGCAGGGAATCCGGATGCTCGGTTATGAGTGAGCAGTGAGTGTGAGCCTCAACATA 60
 DB 1 AGCAGGGAATCCGGATGCTCGGTTATGAGTGAGCAGTGAGTGTGAGCCTCAACATA 60
 QY 61 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATACCAAGTGC 120
 DB 61 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATACCAAGTGC 120
 QY 121 CATCTGAGTGTTCCCTGGCTCTCAAGGGGTAGGCAGTGGCCAGTGCTTCAGCCTG 180
 DB 121 CATCTGAGTGTTCCCTGGCTCTCAAGGGGTAGGCAGTGGCCAGTGCTTCAGCCTG 180
 QY 181 GTGTGCTTCTCATTCTCCATCTGGACCAAGGCTCCTGGTCCAAAGGCTCTTTGGTGCA 240
 DB 181 GTGTGCTTCTCATTCTCCATCTGGACCAAGGCTCCTGGTCCAAAGGCTCTTTGGTGCA 240
 QY 241 GAAGAGCTTTCATCCAGTGTCATGAGCAATATTGGGATCACCTTGTGAGCAAAAG 300
 DB 241 GAAGAGCTTTCATCCAGTGTCATGAGCAATATTGGGATCACCTTGTGAGCAAAAG 300
 QY 301 GCGAACCAAGCAGTCAATTTACAGAACTAAGGAGGCTGTAGGCTGTGGGACTAAGT 360
 DB 301 GCGAACCAAGCAGTCAATTTACAGAACTAAGGAGGCTGTAGGCTGTGGGACTAAGT 360
 QY 361 TTGCGCGCAAGGACCAAGTTCGAAACAGCCTTTGAAAGCTAGCTTTGAACTTGCAGCTAT 420
 DB 361 TTGCGCGCAAGGACCAAGTTCGAAACAGCCTTTGAAAGCTAGCTTTGAACTTGCAGCTAT 420
 QY 421 GGCCTGGTTGAGATGGATTCGTGGTCACTCTAGGATTTAGCCCAACCCCAAGTGTGG 480
 DB 421 GGCCTGGTTGAGATGGATTCGTGGTCACTCTAGGATTTAGCCCAACCCCAAGTGTGG 480

QY 481 AAAAATGGGTGGGTGCTCTGATTTGGAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
 DB 481 AAAAATGGGTGGGTGCTCTGATTTGGAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
 QY 541 TGTTCACCACTCATCTGATFACCTTGGACTAACTCGTCGATTCAGAGAAATTTATCACCAAAA 600
 DB 541 TGTTCACCACTCATCTGATFACCTTGGACTAACTCGTCGATTCAGAGAAATTTATCACCAAAA 600
 QY 601 GATCCCATATTTCAACACTTCAAACTGCAACACACACAGAAATTTATTTGTGAGTGTGAGT 660
 DB 601 GATCCCATATTTCAACACTTCAAACTGCAACACACACAGAAATTTATTTGTGAGTGTGAGT 660
 QY 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCTCTCTGCT 720
 DB 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCTCTCTGCT 720
 QY 721 CCAGCTTCCACTTCTATTTCCACGGAGAAAAATTTGATTTGTGTGTCACAGAAATTTTATG 780
 DB 721 CCAGCTTCCACTTCTATTTCCACGGAGAAAAATTTGATTTGTGTGTCACAGAAATTTTATG 780
 QY 781 GAAACTAGCACCATGCTCTACAGAACTGAACCATTTTGTGAAAAATAAAGCAGCATTTCAAG 840
 DB 781 GAAACTAGCACCATGCTCTACAGAACTGAACCATTTTGTGAAAAATAAAGCAGCATTTCAAG 840
 QY 841 AATGAAGCTGTGGTGGTGGAGGTGTCCTCCACGGCTCTGCTAGTGTCTCTCTCTCTTC 900
 DB 841 AATGAAGCTGTGGTGGTGGAGGTGTCCTCCACGGCTCTGCTAGTGTCTCTCTCTCTTC 900
 QY 901 TTTGTGTGTGAGTGTGCTTGGATTTTGTGCTTATGTGCTGCTGCTGCTGCTGCTGCTGCT 960
 DB 901 TTTGTGTGTGAGTGTGCTTGGATTTTGTGCTTATGTGCTGCTGCTGCTGCTGCTGCTGCT 960
 QY 961 TTTCAACACAGAACTCAGCAGAGGAAATGATCGAAACCAAGATAGTAAAGGAGGAGAG 1020
 DB 961 TTTCAACACAGAACTCAGCAGAGGAAATGATCGAAACCAAGATAGTAAAGGAGGAGAG 1020
 QY 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAATCGATATAAATCCAGAGAGTCC 1080
 DB 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAATCGATATAAATCCAGAGAGTCC 1080
 QY 1081 AAGAGTCAAGCAAAACTACCGTGGATGCTGCTGGAAGTGAAGTTAGATGAGACAGAAA 1140
 DB 1081 AAGAGTCAAGCAAAACTACCGTGGATGCTGCTGGAAGTGAAGTTAGATGAGACAGAAA 1140
 QY 1141 TGAGAGACACACTGAGGCTGTTCTTTCATGCTCTTACCTGCTGCTGCTGCTGCTGCTG 1200
 DB 1141 TGAGAGACACACTGAGGCTGTTCTTTCATGCTCTTACCTGCTGCTGCTGCTGCTGCTG 1200
 QY 1201 ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTTGTCTTAACTGGAATCAGC 1260
 DB 1201 ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTTGTCTTAACTGGAATCAGC 1260
 QY 1261 TCAGAGCTGCCATTTGGAATGATGAGTGACCAAGAGAAATGCTCTCTCTTATTTGTAAC 1320
 DB 1261 TCAGAGCTGCCATTTGGAATGATGAGTGACCAAGAGAAATGCTCTCTCTTATTTGTAAC 1320
 QY 1321 CCTGTCTGATCTTATCTCTTACCTCCAAAGTTCCTCCAGGCTCTTCTAGCCTGGCTAT 1380
 DB 1321 CCTGTCTGATCTTATCTCTTACCTCCAAAGTTCCTCCAGGCTCTTCTAGCCTGGCTAT 1380
 QY 1381 GTCTTAATTAATCCACTGGGAGAAAGAGTTTTCGAAAGTGAAGGACCTTAAACATC 1440
 DB 1381 GTCTTAATTAATCCACTGGGAGAAAGAGTTTTCGAAAGTGAAGGACCTTAAACATC 1440
 QY 1441 TCATCAGTATCCAGTGGTAAAAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 DB 1441 TCATCAGTATCCAGTGGTAAAAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 QY 1501 CAAAGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCTTTCTTCA 1560
 DB 1501 CAAAGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCTTTCTTCA 1560

Qy	1561	GCTCTGAAAGAGAAACACGTTATCCCACTGACATGTCTCTCTGAGCCCGGTAGAGCAAA	1620
Db	1561	GCTCTGAAAGAGAAACACGTTATCCCACTGACATGTCTCTCTGAGCCCGGTAGAGCAAA	1620
Qy	1621	AGAATGGCAGAAAAAGTTTGTAGCCCTGTAAGAGCCATGGAGATTCTTCATAACTTTGAGACCTAA	1680
Db	1621	AGAATGGCAGAAAAAGTTTGTAGCCCTGTAAGAGCCATGGAGATTCTTCATAACTTTGAGACCTAA	1680
Qy	1681	TCTCTGTAAAGCTAAAAATAAGAAATAAGAACAGGCTGAGGATACGACAGTACATGTCTCA	1740
Db	1681	TCTCTGTAAAGCTAAAAATAAGAAATAAGAACAGGCTGAGGATACGACAGTACATGTCTCA	1740
Qy	1741	GCAGGACTGTAAACACAGACAGGCTCAAGTGTCTTCTCTGACACATTTGAGTTGGAAT	1800
Db	1741	GCAGGACTGTAAACACAGACAGGCTCAAGTGTCTTCTCTGACACATTTGAGTTGGAAT	1800
Qy	1801	CACGTGTTTAGAACACACACACTTACTTTTTTCTGGTCTCTACCACCTGCTGATATTTTCTCT	1860
Db	1801	CACGTGTTTAGAACACACACACTTACTTTTTTCTGGTCTCTACCACCTGCTGATATTTTCTCT	1860
Qy	1861	AGGAAATATACTTTTACAAGTAAACAAAAATAAAACTCTTTATATAAATTTCTATTTTATCT	1920
Db	1861	AGGAAATATACTTTTACAAGTAAACAAAAATAAAACTCTTTATATAAATTTCTATTTTATCT	1920
Qy	1921	GAGTTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA	1980
Db	1921	GAGTTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA	1980
Qy	1981	TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTCTGCAAGCTATTACACTC	2040
Db	1981	TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTCTGCAAGCTATTACACTC	2040
Qy	2041	TGTAATTTGAATATTATTTCTCTCAAAAAATGCAATAGTAAGACGCTATCTGGGAAGCTAT	2100
Db	2041	TGTAATTTGAATATTATTTCTCTCAAAAAATGCAATAGTAAGACGCTATCTGGGAAGCTAT	2100
Qy	2101	TTTTTTTCAGTTTGTATATTTCTAGCTTACTCTCTTCCAAACTAATTTTATTTTTCGTGA	2160
Db	2101	TTTTTTTCAGTTTGTATATTTCTAGCTTACTCTCTTCCAAACTAATTTTATTTTTCGTGA	2160
Qy	2161	GACTTAATCTTATTTCTTAATATGCAACCACTTATAACCTTAATTTATTTATTAAC	2220
Db	2161	GACTTAATCTTATTTCTTAATATGCAACCACTTATAACCTTAATTTATTTATTAAC	2220
Qy	2221	ATACCTTAAGAAGTACATTTGTTACTCTTATATACCAAGGACATTTTAAAAAGTGCATTAA	2280
Db	2221	ATACCTTAAGAAGTACATTTGTTACTCTTATATACCAAGGACATTTTAAAAAGTGCATTAA	2280
Qy	2281	CAAAATGTATCACTAGCCCTCTTTTCCAAACAAGGGACTGAGAGATCGAAAAATATT	2340
Db	2281	CAAAATGTATCACTAGCCCTCTTTTCCAAACAAGGGACTGAGAGATCGAAAAATATT	2340
Qy	2341	TGTGCAAAAAATTAAGGCAATTTAGAAAACTTT	2372
Db	2341	TGTGCAAAAAATTAAGGCAATTTAGAAAACTTT	2372

RESULT 9

ACA58457

ID ACA58457 standard; cDNA: 2372 BP.

XX

ACA

XX

DT 10-JUN-2003 (first entry)

XX

DE cDN.

XX

KW Hum.

KW Alz.

KW neu

XX 8

OS Hom.

PN	US2002192659-A1.
XX	
PD	19-DEC-2002.
XX	
XX	
PF	10-JUL-2001; 2001US-000202853
XX	
PR	17-SEP-1997; 97US-0059113P
PR	17-SEP-1997; 97US-0059115P
PR	17-SEP-1997; 97US-0059117P
PR	17-SEP-1997; 97US-0059119P
PR	17-SEP-1997; 97US-0059121P
PR	17-SEP-1997; 97US-0059122P
PR	17-SEP-1997; 97US-0059184P
PR	18-SEP-1997; 97US-0059263P
PR	18-SEP-1997; 97US-0059266P
PR	15-OCT-1997; 97US-0062125P
PR	17-OCT-1997; 97US-0062285P
PR	17-OCT-1997; 97US-0062287P
PR	21-OCT-1997; 97US-0062348P
PR	24-OCT-1997; 97US-0062814P
PR	24-OCT-1997; 97US-0063161P
PR	24-OCT-1997; 97US-0063045P
PR	24-OCT-1997; 97US-0063120P
PR	24-OCT-1997; 97US-0063121P
PR	24-OCT-1997; 97US-0063127P
PR	24-OCT-1997; 97US-0063128P
PR	27-OCT-1997; 97US-0063327P
PR	27-OCT-1997; 97US-0063329P
PR	28-OCT-1997; 97US-0063541P
PR	28-OCT-1997; 97US-0063542P
PR	28-OCT-1997; 97US-0063544P
PR	28-OCT-1997; 97US-0063549P
PR	28-OCT-1997; 97US-0063550P
PR	28-OCT-1997; 97US-0063564P
PR	29-OCT-1997; 97US-0063435P
PR	29-OCT-1997; 97US-0063704P
PR	29-OCT-1997; 97US-0064103P
PR	30-NOV-1997; 97US-0064248P
PR	29-OCT-1997; 97US-0063735P
PR	29-OCT-1997; 97US-0064809P
PR	29-OCT-1997; 97US-0063728P
PR	29-OCT-1997; 97US-0064215P
PR	31-OCT-1997; 97US-0063870P
PR	31-OCT-1997; 97US-0066120P
PR	30-NOV-1997; 97US-0064103P
PR	24-NOV-1997; 97US-0066365P
PR	24-NOV-1997; 97US-0066453P
PR	24-NOV-1997; 97US-0066466P
PR	24-NOV-1997; 97US-0066511P
PR	24-NOV-1997; 97US-0066770P
PR	24-NOV-1997; 97US-0066772P
PR	10-SEP-1998; 98WO-US018824.
PR	14-SEP-1998; 98WO-US019177.
PR	16-SEP-1998; 98WO-US019330.
PR	17-SEP-1998; 98WO-US019437.
PR	01-DEC-1998; 98WO-US0205108.
PR	08-SEP-1999; 99WO-US020594.
PR	13-SEP-1999; 99WO-US020944.
PR	15-SEP-1999; 99WO-US020190.
PR	15-SEP-1999; 99WO-US021547.
PR	03-OCT-1999; 99WO-US023089.
PR	29-NOV-1999; 99WO-US028214.
PR	30-NOV-1999; 99WO-US028313.
PR	01-DEC-1999; 99WO-US028301.
PR	02-DEC-1999; 99WO-US028564.
PR	02-DEC-1999; 99WO-US028565.
PR	16-DEC-1999; 99WO-US030095.
PR	20-DEC-1999; 99WO-US030911.
PR	20-DEC-1999; 99WO-US030999.

05-JAN-2000; 2000WO-US000219.
 11-FEB-2000; 2000WO-US003565.
 22-FEB-2000; 2000WO-US004414.
 24-FEB-2000; 2000WO-US005004.
 02-MAR-2000; 2000WO-US005841.
 20-MAR-2000; 2000WO-US007377.
 30-MAR-2000; 2000WO-US008439.
 22-MAY-2000; 2000WO-US014042.
 02-JUN-2000; 2000WO-US015264.
 28-JUL-2000; 2000WO-US020710.
 24-AUG-2000; 2000WO-US023328.
 18-SEP-2000; 2000US-00665350.
 (GETH) GENENTECH INC.
 Askenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini IJ;
 Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 Williams EM, Wood WI;
 WPI; 2003-361832/34.
 P-PSDB; AB071480.
 New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
 PRO1869, useful in molecular biology, chromosome and gene mapping, in
 generating antisense RNA and DNA, and in gene therapy.
 Claim 2; Fig 73; 474pp; English.
 The present invention relates to the isolation of novel human secreted
 and transmembrane proteins (PRO polypeptides), and the polynucleotide
 sequences encoding them. The polynucleotide sequences are useful in
 molecular biology, as hybridisation probes, in chromosome and gene
 mapping, in generating antisense RNA and DNA, and in gene therapy. The
 polynucleotide sequences may also be used in preparing PRO polypeptides
 by recombinant techniques, and in generating either transgenic animals or
 knock-out animals which, in turn, are useful in the development and
 screening of therapeutically useful reagents. The PRO polypeptides or
 their antibodies are useful in preparing a medicament for treating a
 condition responsive to the polypeptide or antibody, such as cancer, the
 Alzheimer's disease or ischaemia, and in various diagnostic assays. The
 present sequence encodes a human PRO polypeptide of the invention
 Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2372; DB 7; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 AGCAGGAAATCCGATGCTCGGTATGAAGTGGAGAGTGGAGTGGAGCTCAACATA 60
 1 AGCAGGAAATCCGATGCTCGGTATGAAGTGGAGAGTGGAGTGGAGCTCAACATA 60
 61 GTTCAGAACTCTCCATCCGAGTATGTTATGAGCATCTGCTCTCATATCACCAGTGGC 120
 61 GTTCAGAACTCTCCATCCGAGTATGTTATGAGCATCTGCTCTCATATCACCAGTGGC 120
 121 CATCTGAGTGTTCCTCGGCTCTCAAGGGTGGAGCATGATGGCCAGGTCTTCAGCTG 180
 121 CATCTGAGTGTTCCTCGGCTCTCAAGGGTGGAGCATGATGGCCAGGTCTTCAGCTG 180
 181 GTGTGCTTCTCATTCTCCATCTGGACACGAGGCTCTGCTGCTCAAGGCTCTTTCGGTGA 240
 181 GTGTGCTTCTCATTCTCCATCTGGACACGAGGCTCTGCTGCTCAAGGCTCTTTCGGTGA 240
 241 GAAGAGCTTTCATCCAGGTGTCATGAGAAATATGGGATCACCTTGTGAGCAAAAAG 300
 241 GAAGAGCTTTCATCCAGGTGTCATGAGAAATATGGGATCACCTTGTGAGCAAAAAG 300
 301 GCGAACCCAGCTCAATTTACAGAGCTAAGAGGCTGTAGGCTGCTGGAGCTTAAGT 360
 301 GCGAACCCAGCTCAATTTACAGAGCTAAGAGGCTGTAGGCTGCTGGAGCTTAAGT 360

QY 361 TTGCGCGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTTCAGCTAT 420
 DB 361 TTGCGCGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTTCAGCTAT 420
 QY 421 GCGTGGGTGGAGATGAGATTCGTGTCTATCTCTAGGATAGCCCAAAACCCCAAGTGTGG 480
 DB 421 GCGTGGGTGGAGATGAGATTCGTGTCTATCTCTAGGATAGCCCAAAACCCCAAGTGTGG 480
 QY 481 AAAAATGGGTGGGTGCTCTGATTTGGAGGTTCCAGTGAGCCGACAGTTTTCAGCCCTAT 540
 DB 481 AAAAATGGGTGGGTGCTCTGATTTGGAGGTTCCAGTGAGCCGACAGTTTTCAGCCCTAT 540
 QY 541 TGTACAACTCATCTGATATCTGGAATTAACCTCGTGCATTTCCAGAAATTTATCACCACAAA 600
 DB 541 TGTACAACTCATCTGATATCTGGAATTAACCTCGTGCATTTCCAGAAATTTATCACCACAAA 600
 QY 601 GATCCATATTCACACTCAAACTGCAACACAAACACAGAAATTTATTTGTGAGTACAGT 660
 DB 601 GATCCATATTCACACTCAAACTGCAACACAAACACAGAAATTTATTTGTGAGTACAGT 660
 QY 661 ACCTACTCGGTGGATCCCTTACTCTACAATACCTGCTCCCTACTACTCTCTCTGCT 720
 DB 661 ACCTACTCGGTGGATCCCTTACTCTACAATACCTGCTCCCTACTACTCTCTCTGCT 720
 QY 721 CCAGCTTCCACTTCTATTTCCAGGAGAAAAAATGATTTGTGTGTCACAGAAATTTATG 780
 DB 721 CCAGCTTCCACTTCTATTTCCAGGAGAAAAAATGATTTGTGTGTCACAGAAATTTATG 780
 QY 781 GAACTACAGCATCTCTACAGAACTGAACTGATTTGTTGAAATTAAGCAGCATTCAG 840
 DB 781 GAACTACAGCATCTCTACAGAACTGAACTGATTTGTTGAAATTAAGCAGCATTCAG 840
 QY 841 AATGAAGCTGTGGTGTGGAGGCTCTCCCGCGCTCTGCTAGTCTGCTCTCTCTCTCTC 900
 DB 841 AATGAAGCTGTGGTGTGGAGGCTCTCCCGCGCTCTGCTAGTCTGCTCTCTCTCTC 900
 QY 901 TTTGCTGTGCTGAGCTGTGCTTTGGAATTTGCTATGTCACAAAGGTATGTGAAGCTTCCCT 960
 DB 901 TTTGCTGTGCTGAGCTGTGCTTTGGAATTTGCTATGTCACAAAGGTATGTGAAGCTTCCCT 960
 QY 961 TTTCAACACAGATCAGCAGAGGAAATGATCGAAACCAAAGTATGTAAGGAGAGAG 1020
 DB 961 TTTCAACACAGATCAGCAGAGGAAATGATCGAAACCAAAGTATGTAAGGAGAGAG 1020
 QY 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAATCTGATAAAACCCAGAGAGTCC 1080
 DB 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAATCTGATAAAACCCAGAGAGTCC 1080
 QY 1081 AAGAGTCCCAAGCAAACTACCGTGGATGCTGGAAGCTGAAATTTAGATGAGACAGAAA 1140
 DB 1081 AAGAGTCCCAAGCAAACTACCGTGGATGCTGGAAGCTGAAATTTAGATGAGACAGAAA 1140
 QY 1141 TGAGAGACACACTGAGGCTGGTTTCTTCTGATGCTCTTACCTGCTCCCTGCTGGGAA 1200
 DB 1141 TGAGAGACACACTGAGGCTGGTTTCTTCTGATGCTCTTACCTGCTCCCTGCTGGGAA 1200
 QY 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCCTTAAGTGAATCAGC 1260
 DB 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCCTTAAGTGAATCAGC 1260
 QY 1261 TCAGGACTGCCATTTGGAATGAGTGCACCAAGAGAAATGCCCTTCTCTTTATTGTAAC 1320
 DB 1261 TCAGGACTGCCATTTGGAATGAGTGCACCAAGAGAAATGCCCTTCTCTTTATTGTAAC 1320
 QY 1321 CTTGCTGATCTATCTCTTACCTCCAAAGCTTCCAGGCTTCTTAGCTGCTGCTAT 1380
 DB 1321 CTTGCTGATCTATCTCTTACCTCCAAAGCTTCCAGGCTTCTTAGCTGCTGCTAT 1380
 QY 1381 GTCTTAATAATATCCCACTGGGAGAAAGAGTGTGTAAGTGCAGGACCTTAAACATC 1440
 DB 1381 GTCTTAATAATATCCCACTGGGAGAAAGAGTGTGTAAGTGCAGGACCTTAAACATC 1440

QY 1441 TCATCAGTATCCAGTGGTAAAGGCTCTGGCTGTCTGAGGCTAGTGGTTGAAAGC 1500
Db |||||||
1441 TCATCAGTATCCAGTGGTAAAGGCTCTGGCTGTCTGAGGCTAGTGGTTGAAAGC 1500
QY 1501 CAAGGAGTCTAGAGCAAGGCTTCTCTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
Db |||||||
1501 CAAGGAGTCTAGAGCAAGGCTTCTCTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
QY 1561 GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTCTCTGAGCGGCTAAGAGCAA 1620
Db |||||||
1561 GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTCTCTGAGCGGCTAAGAGCAA 1620
QY 1621 AGAATGCGAGAAAGTTAGCCCTGAAAGCCATGAGATTCCTCATTAACCTTGAGACCTAA 1680
Db |||||||
1621 AGAATGCGAGAAAGTTAGCCCTGAAAGCCATGAGATTCCTCATTAACCTTGAGACCTAA 1680
QY 1681 TCTCTGTAAGCTTAAATAAGAAATAGAACAGGCTGAGATACGACAGTACACTGCA 1740
Db |||||||
1681 TCTCTGTAAGCTTAAATAAGAAATAGAACAGGCTGAGATACGACAGTACACTGCA 1740
QY 1741 GCAGGGACTCTAAACACAGACAGGCTCAAGTGTCTCTGACATGCTGATATTTCTCT 1800
Db |||||||
1741 GCAGGGACTCTAAACACAGACAGGCTCAAGTGTCTCTGACATGCTGATATTTCTCT 1800
QY 1801 CACTGTTTGAACAACACACTTACTTTTCTGTCTCTACCACTGCTGATATTTCTCT 1860
Db |||||||
1801 CACTGTTTGAACAACACACTTACTTTTCTGTCTCTACCACTGCTGATATTTCTCT 1860
QY 1861 AGGAATATATCTTTTACAAGTACCAAAATATAAACTCTTATAAATTTCTATTTATCT 1920
Db |||||||
1861 AGGAATATATCTTTTACAAGTACCAAAATATAAACTCTTATAAATTTCTATTTATCT 1920
QY 1921 GAGTTACAGAAATGATTTACTAAGGAGTACTCAGTAATTTGTTTAAAGTAATAAAA 1980
Db |||||||
1921 GAGTTACAGAAATGATTTACTAAGGAGTACTCAGTAATTTGTTTAAAGTAATAAAA 1980
QY 1981 TTCAACAAACATTTGCTGAATAGTACTATATGTCAAGTCTGTGCAAGGTATTACACTC 2040
Db |||||||
1981 TTCAACAAACATTTGCTGAATAGTACTATATGTCAAGTCTGTGCAAGGTATTACACTC 2040
QY 2041 TGTAATGTAATATTTCTCAAAAATTCGACATAGTAGAAGCTATCTGGGAAGCTAT 2100
Db |||||||
2041 TGTAATGTAATATTTCTCAAAAATTCGACATAGTAGAAGCTATCTGGGAAGCTAT 2100
QY 2101 TTTTTCAGTTTGTATTTCTAGCTTATCTTCTCCAACTAATTTTATTTTCTGCTGA 2160
Db |||||||
2101 TTTTTCAGTTTGTATTTCTAGCTTATCTTCTCCAACTAATTTTATTTTCTGCTGA 2160
QY 2161 GACTAATCTTATTTCAATTTCTTAATATGCAACCACTTATACTTAATTTATTTAAAC 2220
Db |||||||
2161 GACTAATCTTATTTCAATTTCTTAATATGCAACCACTTATACTTAATTTATTTAAAC 2220
QY 2221 ATACCTAAGAGTACATTTGTTACTCTATATACCAAGCAATTTTAAAGTCCCATTA 2280
Db |||||||
2221 ATACCTAAGAGTACATTTGTTACTCTATATACCAAGCAATTTTAAAGTCCCATTA 2280
QY 2281 CAATGTTATCAGTACGCTCTCTTTTCCAAACAGAGGAGCTGAGAGTCCAGAAATTT 2340
Db |||||||
2281 CAATGTTATCAGTACGCTCTCTTTTCCAAACAGAGGAGCTGAGAGTCCAGAAATTT 2340
QY 2341 TGTGACAAAAAATTAAGCATTTTGAAGAACTT 2372
Db |||||||
2341 TGTGACAAAAAATTAAGCATTTTGAAGAACTT 2372

RESULT 10

ACA60164

ID ACA60164 standard; cDNA; 2372 BP.

XX ACA60164;

AC ACA60164;

XX ACA60164;

DT 12-JUN-2003 (first entry)

XX

Human cDNA for secreted/transmembrane protein PRO263.
Human; ss; gene; secreted protein; transmembrane protein; PRO;
gene therapy; chromosome identification; chromosome marker.

Homo sapiens.

US2003003530-A1.

02-JAN-2003.

11-JUL-2001; 2001US-00904011.

17-SEP-1997; 97US-0059113P.

17-SEP-1997; 97US-0059115P.

17-SEP-1997; 97US-0059117P.

17-SEP-1997; 97US-0059119P.

17-SEP-1997; 97US-0059121P.

17-SEP-1997; 97US-0059122P.

17-SEP-1997; 97US-0059184P.

18-SEP-1997; 97US-0059263P.

18-SEP-1997; 97US-0059266P.

15-OCT-1997; 97US-0062125P.

17-OCT-1997; 97US-0062285P.

17-OCT-1997; 97US-0062287P.

21-OCT-1997; 97US-0063486P.

24-OCT-1997; 97US-0062814P.

24-OCT-1997; 97US-0062816P.

24-OCT-1997; 97US-0063045P.

24-OCT-1997; 97US-0063120P.

24-OCT-1997; 97US-0063121P.

24-OCT-1997; 97US-0063127P.

24-OCT-1997; 97US-0063128P.

27-OCT-1997; 97US-0063327P.

27-OCT-1997; 97US-0063329P.

28-OCT-1997; 97US-0063541P.

28-OCT-1997; 97US-0063542P.

28-OCT-1997; 97US-0063549P.

28-OCT-1997; 97US-0063550P.

28-OCT-1997; 97US-0063564P.

29-OCT-1997; 97US-0063435P.

29-OCT-1997; 97US-0063738P.

29-OCT-1997; 97US-0063704P.

29-OCT-1997; 97US-0063732P.

29-OCT-1997; 97US-0063734P.

29-OCT-1997; 97US-0063735P.

29-OCT-1997; 97US-0063738P.

29-OCT-1997; 97US-0064215P.

31-OCT-1997; 97US-0063870P.

31-OCT-1997; 97US-0064103P.

03-NOV-1997; 97US-0064248P.

07-NOV-1997; 97US-0064809P.

12-NOV-1997; 97US-0065186P.

17-NOV-1997; 97US-0065846P.

18-NOV-1997; 97US-0065693P.

21-NOV-1997; 97US-0066120P.

21-NOV-1997; 97US-0066364P.

24-NOV-1997; 97US-0066453P.

24-NOV-1997; 97US-0066466P.

24-NOV-1997; 97US-0066511P.

24-NOV-1997; 97US-0066770P.

24-NOV-1997; 97US-0066772P.

10-SEP-1998; 98WO-US018824.

14-SEP-1998; 98WO-US019177.

16-SEP-1998; 98WO-US019330.

17-SEP-1998; 98WO-US019437.

01-DEC-1998; 98WO-US025108.

08-SEP-1999; 99WO-US020594.

13-SEP-1999; 99WO-US020944.

15-SEP-1999; 99WO-US021090.

15-SEP-1999; 99WO-US021547.

05-OCT-1999; 99WO-US023089.

29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028564.
 PR 16-DEC-1999; 99WO-US028565.
 PR 20-DEC-1999; 99WO-US030911.
 PR 05-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015284.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WL;
 XX
 WPI; 2003-329602/31.
 DR P-PSDB; ABU71926.
 DR
 XX
 PT New transmembrane polypeptides and nucleic acids encoding the
 PT polypeptides, useful in gene therapy, in chromosome identification, as
 PT chromosome markers, in generating probes and in tissue typing.
 XX
 PS
 PS Claim 2; Fig 73; 484pp; English.
 PS
 CC The invention relates to an isolated nucleic acid with at least 80%
 CC nucleic acid sequence identity to a nucleotide sequence encoding one of
 CC 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
 CC PRO protein extracellular domain. Also included are a vector comprising
 CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO
 CC polypeptide (by culturing the host cell for the expression of the PRO
 CC polypeptide, and recovering the PRO polypeptide from the cell culture),
 CC an isolated PRO polypeptide (having at least 80% sequence identity to:
 CC a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
 CC acid sequence encoded by a nucleic acid molecule deposited with an ATCC
 CC number (detailed in the specification); or (c) an extracellular domain of
 CC a PRO polypeptide or to a PRO polypeptide lacking its associated signal
 CC peptide), a chimeric molecule comprising a PRO polypeptide of fused to a
 CC heterologous amino acid sequence, an anti-PRO antibody, detecting a
 CC PRO245 or PRO1868 in a sample suspected of containing the polypeptide,
 CC linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and
 CC modulating at least one biological activity of a cell expressing a PRO245
 CC or PRO1868. Nucleic acids which encode PRO can be used to generate either
 CC transgenic animals or knock-out animals which may be used in the
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy, in chromosome identification, as
 CC chromosome markers, or in generating probes. The PRO polypeptides are
 CC useful as molecular markers for protein electrophoresis, and the isolated
 CC nucleic acids may be used for recombinantly expressing those markers. The
 CC PRO polypeptides and nucleic acids may also be used in tissue typing.
 CC Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. The present sequence encodes a PRO protein
 XX
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2372; DB 7; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 AGCAGGGAAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAGTGGACCTCAACATA 60

1 AGCAGGGAAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAGTGGACCTCAACATA 60
 61 GTTCAGAACTCTCCATCCGAGTAGTTATTAGCATCTGCTCTCATATCAACAGTGGC 120
 61 GTTCAGAACTCTCCATCCGAGTAGTTATTAGCATCTGCTCTCATATCAACAGTGGC 120
 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCAGGTGCTTCAGCCTG 180
 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCAGGTGCTTCAGCCTG 180
 181 GTGTTGCTTCTCATCTCCATCTGACACGAGGCTCTGGTCCAGGCTCTTTGGGTGCA 240
 181 GTGTTGCTTCTCATCTCCATCTGACACGAGGCTCTGGTCCAGGCTCTTTGGGTGCA 240
 241 GAAGAGCTTTCCATCCAGGTGTGATGAGAAATTATGGGGATCACCTTTGTGAGCAAAAAG 300
 241 GAAGAGCTTTCCATCCAGGTGTGATGAGAAATTATGGGGATCACCTTTGTGAGCAAAAAG 300
 301 GCGAACACAGCAGCTGAATTTACAGAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGT 360
 301 GCGAACACAGCAGCTGAATTTACAGAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGT 360
 361 TTGGCCGGCAGGACCAAGTTGAAACAGCCTTGAAGTAGCTTTGAACTTGCAGCTAT 420
 361 TTGGCCGGCAGGACCAAGTTGAAACAGCCTTGAAGTAGCTTTGAACTTGCAGCTAT 420
 421 GCGTGGGTGGAGATGGAATTTGCTGCTCATCTAGGATTAGCCCAAAACCCCAAGTGTGG 480
 421 GCGTGGGTGGAGATGGAATTTGCTGCTCATCTAGGATTAGCCCAAAACCCCAAGTGTGG 480
 481 AAAAAATGGGGTGGGTGCTCTGATTTGGAGGTTCCAGTGGAGCCGACAGTTTCAGCCTAT 540
 481 AAAAAATGGGGTGGGTGCTCTGATTTGGAGGTTCCAGTGGAGCCGACAGTTTCAGCCTAT 540
 541 TGTTACAACTCATCTGATGACTTGGACTAATCTGTCGATTCAGAAATATATCAACCAAAA 600
 541 TGTTACAACTCATCTGATGACTTGGACTAATCTGTCGATTCAGAAATATATCAACCAAAA 600
 601 GATCCCATATTCACACACTCAAACTGCAACACAAACAAAGAAATTTATTTGTCAGTGACAGT 660
 601 GATCCCATATTCACACACTCAAACTGCAACACAAACAAAGAAATTTATTTGTCAGTGACAGT 660
 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCTCTCTGCT 720
 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCTCTCTGCT 720
 721 CCAGCTTCCACTTCTATTTCCAGGAGAAAATTTGATTTGTGTACAGAAAGTTTATG 780
 721 CCAGCTTCCACTTCTATTTCCAGGAGAAAATTTGATTTGTGTACAGAAAGTTTATG 780
 781 GAAACTAGCACCATGCTACAGAAACTGAAACCATTTGTTGAAAATAAAGCAGCAATCAAG 840
 781 GAAACTAGCACCATGCTACAGAAACTGAAACCATTTGTTGAAAATAAAGCAGCAATCAAG 840
 841 AATGAAGCTGTGGGTGGAGGTGTCACAGGCTCTGCTAGTGTGCTCTCTCTCTCTC 900
 841 AATGAAGCTGTGGGTGGAGGTGTCACAGGCTCTGCTAGTGTGCTCTCTCTCTCTC 900
 901 TTGTTGCTGACAGTGGTCTTGGATTTTCTATGTCATAAGGTATGTGAAGGCTTCCCT 960
 901 TTGTTGCTGACAGTGGTCTTGGATTTTCTATGTCATAAGGTATGTGAAGGCTTCCCT 960
 961 TTATACAAACAGAAATCAGCAGAAAGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAAG 1020
 961 TTATACAAACAGAAATCAGCAGAAAGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAAG 1020
 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAATCTGATATAAAACCCAGAGAGTCC 1080
 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAATCTGATATAAAACCCAGAGAGTCC 1080
 1081 AAGAGTCCAAAGCAAAACTACCGTGGATGCTGCTGGAAGCTGGAAGTTAGATGACACAGAAA 1140

29-OCT-1997; 97US-0063735P.
29-OCT-1997; 97US-0063738P.
29-OCT-1997; 97US-0064215P.
31-OCT-1997; 97US-0063870P.
31-OCT-1997; 97US-0064103P.
03-NOV-1997; 97US-0064248P.
07-NOV-1997; 97US-0064809P.
12-NOV-1997; 97US-0065186P.
17-NOV-1997; 97US-0065848P.
18-NOV-1997; 97US-0065693P.
21-NOV-1997; 97US-0066120P.
21-NOV-1997; 97US-0066364P.
24-NOV-1997; 97US-0066453P.
24-NOV-1997; 97US-0066466P.
24-NOV-1997; 97US-0066511P.
24-NOV-1997; 97US-0066770P.
24-NOV-1997; 97US-0066772P.
10-SEP-1998; 98WO-US018824.
14-SEP-1998; 98WO-US019177.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98WO-US019437.
01-DEC-1998; 98WO-US025108.
08-SEP-1999; 99WO-US020594.
13-SEP-1999; 99WO-US020944.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
05-OCT-1999; 99WO-US023089.
29-NOV-1999; 99WO-US028214.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
02-DEC-1999; 99WO-US028564.
02-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
20-DEC-1999; 99WO-US030999.
05-JAN-2000; 2000WO-US000219.
11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
30-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
XX
FA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski EJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-370793/35.
DR P-PSDB; ABO01809.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
PT PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,
PT cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
PT or strokes.
XX
PS Claim 2; Fig 73; 482pp; English.
XX
CC The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence
CC with at least 80% identity to a DNA encoding a PRO polypeptide comprising
CC any of 61 sequences having 164-1119 amino acids fully defined in the
CC specification. The PRO polypeptides or polynucleotides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. These are

CC particularly useful for detecting or treating e.g. Parkinson's disease,
CC Alzheimer's disease, inflammations, nephritis, wound healing, nerve
CC repair, collateral blood vessel formation, cancers (e.g. colorectal
CC cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
CC arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
CC restenosis, dermal fibrotic conditions (e.g. keloids or scarring), or
CC ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
CC infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
CC pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
CC therapeutic intervention in these diseases, and diagnostic determination
CC of the presence of these diseases. The PRO polypeptides are also useful
CC as molecular weight markers, or for chromosome identification. The PRO
CC genes are useful as hybridisation probes, or for screening libraries of
CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. This sequence
CC encodes a novel human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
Query Match 100.0%; Score 2372; DB 7; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCAGGAAATCCGGATGCTCTCGGTTATGAAGTGGAGCAGTGAGTGCCTCAACATA 60
DB 1 AGCAGGAAATCCGGATGCTCTCGGTTATGAAGTGGAGCAGTGAGTGCCTCAACATA 60
QY 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTCAGCATCTGCTCTCATATCACAGTGGC 120
DB 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTCAGCATCTGCTCTCATATCACAGTGGC 120
QY 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
DB 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
QY 181 GTGTTGCTTCTCACTTCCATCTGAGCAGAGGCTCTGTTCCAGGCTCTTTGGGTGCA 240
DB 181 GTGTTGCTTCTCACTTCCATCTGAGCAGAGGCTCTGTTCCAGGCTCTTTGGGTGCA 240
QY 241 GAAGAGCTTCCATCCAGGTGTCATGCAGAAATATGGGATATTCAGGCTTGTGAGCAAAAG 300
DB 241 GAAGAGCTTCCATCCAGGTGTCATGCAGAAATATGGGATATTCAGGCTTGTGAGCAAAAG 300
QY 301 GCGAACCAAGCAGCTGAATTTACAGAGCTAAGAGGCTGTAGGCTGCTGGAGCTAAGT 360
DB 301 GCGAACCAAGCAGCTGAATTTACAGAGCTAAGAGGCTGTAGGCTGCTGGAGCTAAGT 360
QY 361 TTGGCCGCAAGGACCAAGTTGAAACAGCTTGAAGCTAGCTTTGAAACTTGCAGCTAT 420
DB 361 TTGGCCGCAAGGACCAAGTTGAAACAGCTTGAAGCTAGCTTTGAAACTTGCAGCTAT 420
QY 421 GGCTGGGTGGAGATGGATTCGTGCTCATCTCTAGATTAGCCAAACCCCAAGTGGG 480
DB 421 GGCTGGGTGGAGATGGATTCGTGCTCATCTCTAGATTAGCCAAACCCCAAGTGGG 480
QY 481 AAAAATGGGTGGGTGCTCTGATTTTGAAGGTTTCAAGTGAGCCGACAGTTTGCAGCTAT 540
DB 481 AAAAATGGGTGGGTGCTCTGATTTTGAAGGTTTCAAGTGAGCCGACAGTTTGCAGCTAT 540
QY 541 TGTTCACTCATCTGATCTTGGATTAACCTGCTGCTCATCTAGATTAGCCAAACCCCAAGTGGG 600
DB 541 TGTTCACTCATCTGATCTTGGATTAACCTGCTGCTCATCTAGATTAGCCAAACCCCAAGTGGG 600
QY 601 GATCCCATTTCAACACTCAAACTGCAACAAACAAACAGAAATTTATTTGTCAGTGACAGT 660
DB 601 GATCCCATTTCAACACTCAAACTGCAACAAACAAACAGAAATTTATTTGTCAGTGACAGT 660
QY 661 ACCTACTCGGTGGATCCCTTACTCTCAATACCTGCTGCTTACTACTACTCTCTCTGCT 720
DB 661 ACCTACTCGGTGGATCCCTTACTCTCAATACCTGCTGCTTACTACTACTCTCTCTGCT 720
QY 721 CCAGTTTCCACTTCTATTTCCAGGAGAAATTTGATTTGTCACAGAACTTTTANG 780
DB 721 CCAGTTTCCACTTCTATTTCCAGGAGAAATTTGATTTGTCACAGAACTTTTANG 780

Db 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATTTCGTGCACAGAAATTTTATG 780
QY 781 GAAACTAGCACCANGTCTACAGAACTCAACCAATTTGTTGAAATTAAGAGCAATTCAG 840
Db 781 GAAACTAGCACCANGTCTACAGAACTCAACCAATTTGTTGAAATTAAGAGCAATTCAG 840
QY 841 AATGAAGCTGTGGGTGTTGGAGGTGTCGCCACGGCTCTGCTAGTGTCTCTCTCTTC 900
Db 841 AATGAAGCTGTGGGTGTTGGAGGTGTCGCCACGGCTCTGCTAGTGTCTCTCTCTTC 900
QY 901 TTTGGTGTGAGCTGTGCTTTGGATTTTGTCTATGTCATAAGTATGTAAGAGGCTTCCT 960
Db 901 TTTGGTGTGAGCTGTGCTTTGGATTTTGTCTATGTCATAAGTATGTAAGAGGCTTCCT 960
QY 961 TTTTCAACAGAAATCAGCAAGAAATGATCGAAACCAAGTATGTAAGAGGAGAG 1020
Db 961 TTTTCAACAGAAATCAGCAAGAAATGATCGAAACCAAGTATGTAAGAGGAGAG 1020
QY 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAACTGATAAAACCCAGAGAGTCC 1080
Db 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAACTGATAAAACCCAGAGAGTCC 1080
QY 1081 AAGAGTCCAAAGCAAACTACCGTGCATGCTGGAAGCTGAAGTTTGAATGAGACAGAA 1140
Db 1081 AAGAGTCCAAAGCAAACTACCGTGCATGCTGGAAGCTGAAGTTTGAATGAGACAGAA 1140
QY 1141 TGAGGAGACACCTGAGGCTGTTTCTTTCATGCTCTTACCTGCTGCCAGCTGGGAA 1200
Db 1141 TGAGGAGACACCTGAGGCTGTTTCTTTCATGCTCTTACCTGCTGCCAGCTGGGAA 1200
QY 1201 ATCAAAAGGCGCAAAAGCAAAAGTCCACCTTGTTCTCTAACTGGAATCAGC 1260
Db 1201 ATCAAAAGGCGCAAAAGCAAAAGTCCACCTTGTTCTCTAACTGGAATCAGC 1260
QY 1261 TCAGGAGTGCATGAGCTATGAGTGCAACAAAGAGAGTCCCTTCTCTCTATTTGTAAC 1320
Db 1261 TCAGGAGTGCATGAGCTATGAGTGCAACAAAGAGAGTCCCTTCTCTCTATTTGTAAC 1320
QY 1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCAGGCTTCCAGGCTTCTAGCCTGGCTAT 1380
Db 1321 CCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCAGGCTTCCAGGCTTCTAGCCTGGCTAT 1380
QY 1381 GTCTTAATAATATCCCACTGGGAGAAAGAGTGTTCGAAAGTGCAGAGCACTTAAACATC 1440
Db 1381 GTCTTAATAATATCCCACTGGGAGAAAGAGTGTTCGAAAGTGCAGAGCACTTAAACATC 1440
QY 1441 TCATCAGTATCCAGTGATAAAAGGCTCTCTGCTGTCTGAGGCTAGGTGGTGGTGAAGC 1500
Db 1441 TCATCAGTATCCAGTGATAAAAGGCTCTCTGCTGTCTGAGGCTAGGTGGTGGTGAAGC 1500
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
QY 1561 GCTCTGAAGAGAGAAACACGATCCCACTGACATGTCCTTCTGAGCCCGGTGAAGCAAA 1620
Db 1561 GCTCTGAAGAGAGAAACACGATCCCACTGACATGTCCTTCTGAGCCCGGTGAAGCAAA 1620
QY 1621 AGAATGCGAGAAAGTTTACCCCTGAAAGCCATGGAGATTTCTCATAACTTGAGACCTAA 1680
Db 1621 AGAATGCGAGAAAGTTTACCCCTGAAAGCCATGGAGATTTCTCATAACTTGAGACCTAA 1680
QY 1681 TCTCTGTAAGCTTAAATAAGAAATAGAACAGGCTGAGGATACGACATCACTGTCA 1740
Db 1681 TCTCTGTAAGCTTAAATAAGAAATAGAACAGGCTGAGGATACGACATCACTGTCA 1740
QY 1741 GCAGGAGCTGTAAACACAGACAGGCTCAAGGTGTTTTCTCTGACACATTTGAGTGAAT 1800
Db 1741 GCAGGAGCTGTAAACACAGACAGGCTCAAGGTGTTTTCTCTGACACATTTGAGTGAAT 1800
QY 1801 CACTGTTAGAACACACACACTTACTTTTTCTGCTCTACCACTGCTGATATTTCTCT 1860
Db 1801 CACTGTTAGAACACACACACTTACTTTTTCTGCTCTACCACTGCTGATATTTCTCT 1860

QY 1861 AGGAAATATATCTTTTACAGTAACAAAAATAAAACCTTTATAAATTTCTATTTTATCT 1920
Db 1861 AGGAAATATATCTTTTACAGTAACAAAAATAAAACCTTTATAAATTTCTATTTTATCT 1920
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGTACTCAGTAATTTGTTTAAAAAGTAATAAA 1980
Db 1921 GAGTTACAGAAATGATTACTAAGGAAGTACTCAGTAATTTGTTTAAAAAGTAATAAA 1980
QY 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAGTGTGTCGCAAGGTATTACACTC 2040
Db 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAGTGTGTCGCAAGGTATTACACTC 2040
QY 2041 TGTAAATGAAATATTATTCTTCAAAAAATTCACATAGTAGAACCTATCTGGGAAGCTAT 2100
Db 2041 TGTAAATGAAATATTATTCTTCAAAAAATTCACATAGTAGAACCTATCTGGGAAGCTAT 2100
QY 2101 TTTTTCAGTTCGATATTTCTAGCTTATCTPACCTTCCAAACTAATTTTATTTTGTCTGA 2160
Db 2101 TTTTTCAGTTCGATATTTCTAGCTTATCTPACCTTCCAAACTAATTTTATTTTGTCTGA 2160
QY 2161 GACTAATCTTATTCATTTCTTAATATGCAACCATTTAATTAATTTTATTTTAAAC 2220
Db 2161 GACTAATCTTATTCATTTCTTAATATGCAACCATTTAATTAATTTTATTTTAAAC 2220
QY 2221 ATACCTAAGAGTACATTTGTTACCTCTATATACAAAGCACTTTTAAAGTGCCATTAA 2280
Db 2221 ATACCTAAGAGTACATTTGTTACCTCTATATACAAAGCACTTTTAAAGTGCCATTAA 2280
QY 2281 CAAATGATCACTAGCCCTCTTTTCCAAAGAGGAGTGCAGAGATGCAGAAATATT 2340
Db 2281 CAAATGATCACTAGCCCTCTTTTCCAAAGAGGAGTGCAGAGATGCAGAAATATT 2340
QY 2341 TGTGACAAAAAATTTAAAGCACTTTAGAAAACTT 2372
Db 2341 TGTGACAAAAAATTTAAAGCACTTTAGAAAACTT 2372

RESULT 12
ACA91166
ID ACA91166 standard; cDNA; 2372 BP.
XX ACA91166;
AC ACA91166;
XX
DT 11-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO263 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antibody therapy;
KW pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
XX
OS Homo sapiens.
XX
FN US2003018173-A1.
XX
PD 23-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063515.
XX
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-401702/39.
DR P-PSDB; AB090878.
XX
PT New antibody useful for identifying PRO polypeptides, for affinity
PT purification of PRO polypeptides, and for preparing a medicament for
PT diagnosing or treating conditions responsive to the antibody or PRO
PT polypeptide.

XX Disclosure; Fig 5; 345pp; English.

CC The invention describes an antibody that specifically binds to a PRO

CC polypeptide having a fully defined amino acid sequence given in the

CC specification. The antibody is useful in identifying PRO polypeptides

CC useful for various industrial applications, including pharmaceuticals,

CC diagnostics, biosensors and bioreactors. The antibody is also used for

CC affinity purification of PRO polypeptides from recombinant cell culture

CC or natural sources. The antibody, PRO polypeptide, or its agonists or

CC antagonists, may be used for preparing a medicament for diagnosing or

CC treating a condition responsive to the antibody, PRO polypeptide, or its

CC agonists or antagonists. This sequence encodes a novel human secreted and

CC transmembrane PRO polypeptide

XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 7; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCAGGAAATCCGATCTCTCGTTATCAAGTGGAGCAGTCAAGTGTGAGCCTCAACATA 60

DB |||||

QY 1 AGCAGGAAATCCGATCTCTCGTTATCAAGTGGAGCAGTCAAGTGTGAGCCTCAACATA 60

DB |||||

QY 61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCAACAGTGGC 120

DB |||||

QY 61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCAACAGTGGC 120

DB |||||

QY 121 CATCTGAGTGTTTCCCTGGCTCTGAAGGGTGAAGCAGATGGCCAGGTGCTTCAAGCTG 180

DB |||||

QY 121 CATCTGAGTGTTTCCCTGGCTCTGAAGGGTGAAGCAGATGGCCAGGTGCTTCAAGCTG 180

DB |||||

QY 181 GGTGTTCTTCTCACTTCCATCTGACACAGGCTCTGCTGCTCAAGGCTCTTGTGCTGA 240

DB |||||

QY 181 GGTGTTCTTCTCACTTCCATCTGACACAGGCTCTGCTGCTCAAGGCTCTTGTGCTGA 240

DB |||||

QY 241 GAAGAGCTTTCATCCAGTGTCATGCAGAAATATGGGGATCACCTTGTGAGCAAAAAG 300

DB |||||

QY 241 GAAGAGCTTTCATCCAGTGTCATGCAGAAATATGGGGATCACCTTGTGAGCAAAAAG 300

DB |||||

QY 301 GCGAACACAGCTGAATTTCAACAAGCTAAGAGGCTGTAGGCTGTGGAGCTAAGT 360

DB |||||

QY 301 GCGAACACAGCTGAATTTCAACAAGCTAAGAGGCTGTAGGCTGTGGAGCTAAGT 360

DB |||||

QY 361 TTGGCCGCAAGCAAGTTCGAACAGCTTGAAGCTAGCTTGAACCTTGAACCTTGAACCT 420

DB |||||

QY 361 TTGGCCGCAAGCAAGTTCGAACAGCTTGAAGCTAGCTTGAACCTTGAACCTTGAACCT 420

DB |||||

QY 421 GGTGGGTTGGAGATGGATTCGTGGTCACTCTAGGATAGCCCAACCCCAAGTGTGG 480

DB |||||

QY 421 GGTGGGTTGGAGATGGATTCGTGGTCACTCTAGGATAGCCCAACCCCAAGTGTGG 480

DB |||||

QY 481 AAAAATGGGGTGGTGTCTGATTTTGAAGTTTCCAGTGGAGCGCAGAGTTTGGAGCTAT 540

DB |||||

QY 481 AAAAATGGGGTGGTGTCTGATTTTGAAGTTTCCAGTGGAGCGCAGAGTTTGGAGCTAT 540

DB |||||

QY 541 TGTTAACACTCATCTGATCTTGGACTAATCTGTCATTCAGAAATATCAACCCAAA 600

DB |||||

QY 541 TGTTAACACTCATCTGATCTTGGACTAATCTGTCATTCAGAAATATCAACCCAAA 600

DB |||||

QY 601 GATCCCATATTCACACTCAACTCGAACACACAAACAGAAATATTTGTCAGTGACAGT 660

DB |||||

QY 601 GATCCCATATTCACACTCAACTCGAACACACAAACAGAAATATTTGTCAGTGACAGT 660

DB |||||

QY 661 ACCTACTCGGTGGCATCCCTTACTCTCAATACCTGCCCCCTACTACTCTCTCTCTCT 720

DB |||||

QY 661 ACCTACTCGGTGGCATCCCTTACTCTCAATACCTGCCCCCTACTACTACTCTCTCTCTCT 720

DB |||||

QY 721 CCAGCTTCCACTTCTATTCACGGAGAAATATGATTTGTGTCAACAAGTTTATG 780

DB |||||

QY 721 CCAGCTTCCACTTCTATTCACGGAGAAATATGATTTGTGTCAACAAGTTTATG 780

DB |||||

QY 781 GAAACTAGCACCATGTCTACAGAACTCAACCACTTTTGTGAAAATAAAGCAGCATTCAG 840

DB |||||

QY 781 GAAACTAGCACCATGTCTACAGAACTCAACCACTTTTGTGAAAATAAAGCAGCATTCAG 840

DB |||||

QY 841 AATAGAGCTGTGGTGTGGAGGTGTCCTCCACGGCTCTGCTAGTCTGCTCTCTCTCTTC 900

DB |||||

QY 841 AATAGAGCTGTGGTGTGGAGGTGTCCTCCACGGCTCTGCTAGTCTGCTCTCTCTCTTC 900

DB |||||

QY 901 TTTGTGTCTGAGCTGTGGTCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCTTCCCT 960

DB |||||

QY 901 TTTGTGTCTGAGCTGTGGTCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCTTCCCT 960

DB |||||

QY 961 TTTCAAAACAAGAAATCAGCAGAAAGAAATGATCGAAAACAAAGTATGAAGGAGAGAG 1020

DB |||||

QY 961 TTTCAAAACAAGAAATCAGCAGAAAGAAATGATCGAAAACAAAGTATGAAGGAGAGAG 1020

DB |||||

QY 1021 GCCAATGATACCAACCTTAATCAGGAATCAAGAAACTGATAAAACCCAGAGAGTCC 1080

DB |||||

QY 1021 GCCAATGATACCAACCTTAATCAGGAATCAAGAAACTGATAAAACCCAGAGAGTCC 1080

DB |||||

QY 1081 AAGAGTCCAAAGCAAACTACCGTGCATGCTCGAAGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140

DB |||||

QY 1081 AAGAGTCCAAAGCAAACTACCGTGCATGCTCGAAGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140

DB |||||

QY 1141 TGAGAGACACACCTGAGGCTGTTTCTTTTATGCTCTTACCTGCCCCAGCTGGGAA 1200

DB |||||

QY 1141 TGAGAGACACACCTGAGGCTGTTTCTTTTATGCTCTTACCTGCCCCAGCTGGGAA 1200

DB |||||

QY 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCCTTAACCTGGAATCAGC 1260

DB |||||

QY 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCCTTAACCTGGAATCAGC 1260

DB |||||

QY 1261 TCAGAGCTGCCATTCGAGCTATGGAGTGCACCAAGAGAAATGCCCTTCTCTTATTGTAAAC 1320

DB |||||

QY 1261 TCAGAGCTGCCATTCGAGCTATGGAGTGCACCAAGAGAAATGCCCTTCTCTTATTGTAAAC 1320

DB |||||

QY 1321 CCTGTCTGATCTATCTCTTACCTTCAAAAGCTTCCACGCGCTTCTTACGCTGGCTAT 1380

DB |||||

QY 1321 CCTGTCTGATCTATCTCTTACCTTCAAAAGCTTCCACGCGCTTCTTACGCTGGCTAT 1380

DB |||||

QY 1381 GTCTTAATATATCCACTGGGAGAAAGAGTGTTCGAAAGTCAAGGACCTTAAACATC 1440

DB |||||

QY 1381 GTCTTAATATATCCACTGGGAGAAAGAGTGTTCGAAAGTCAAGGACCTTAAACATC 1440

DB |||||

QY 1441 TCATCAGTATCCAGTGTGTAAGAGGCTCTCTGGCTGTCTGAGGCTAGGTGGTGAAGC 1500

DB |||||

QY 1441 TCATCAGTATCCAGTGTGTAAGAGGCTCTCTGGCTGTCTGAGGCTAGGTGGTGAAGC 1500

DB |||||

QY 1501 CAAGAGTCACTGAGACCAAGGCTTCTCTAATTCGAGCTCAGACCCCTTCTTCA 1560

DB |||||

QY 1501 CAAGAGTCACTGAGACCAAGGCTTCTCTAATTCGAGCTCAGACCCCTTCTTCA 1560

DB |||||

QY 1561 GCTCTGAAGAGAAACAGTATCCACCTGACATGCTTCTGAGCCCGTGAAGCAAA 1620

DB |||||

QY 1561 GCTCTGAAGAGAAACAGTATCCACCTGACATGCTTCTGAGCCCGTGAAGCAAA 1620

DB |||||

QY 1621 AGAATGGCAAGAAAGTTAGCCCTTGAAGCCATGGAGATTCCTATACTTGAAGCCTAA 1680

DB |||||

QY 1621 AGAATGGCAAGAAAGTTAGCCCTTGAAGCCATGGAGATTCCTATACTTGAAGCCTAA 1680

DB |||||

QY 1681 TCTCTGTAAGTAAATAAAGAAATAGAAAGAGTGGAGTATGACAGTACCTGTCA 1740

DB |||||

QY 1681 TCTCTGTAAGTAAATAAAGAAATAGAAAGAGTGGAGTATGACAGTACCTGTCA 1740

DB |||||

QY 1741 GCAGGAGTGAACACACAGAGGCTCAAGGTTTCTCTGAACACTTGAAGTGGAAAT 1800

DB |||||

QY 1741 GCAGGAGTGAACACACAGAGGCTCAAGGTTTCTCTGAACACTTGAAGTGGAAAT 1800

DB |||||

QY 1801 CACTGTTTGAAGACACACACTTACTTTTTTCTGGTCTCTACCACTCTGATATTTCTCT 1860

DB |||||

QY 1801 CACTGTTTGAAGACACACACTTACTTTTTTCTGGTCTCTACCACTCTGATATTTCTCT 1860

DB |||||

QY 1861 AGAATATATCTTTTCAAGTAAACAAATAAATACTTTATTAATTTCTATTTATCT 1920

DB |||||

Db 1861 AGGAAATATATCTTTTACCAAGTAACCAAAAATAAACTCTTATATAATTTCTATTTTATCT 1920
QY 1921 GAGTTACAGAAATGATTTACTAAGGAAGTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
Db 1921 GAGTTACAGAAATGATTTACTAAGGAAGTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
QY 1981 TTCAACAAACATTTGCTGAATAGTACTATATATGTCAAGTGTGCAAGGTATTACACTC 2040
Db 1981 TTCAACAAACATTTGCTGAATAGTACTATATATGTCAAGTGTGCAAGGTATTACACTC 2040
QY 2041 TGTAATTTGAATATTTATTCCTCAAAAAATTCACATAGTAGAAGCTATCTGGGAAGCTAT 2100
Db 2041 TGTAATTTGAATATTTATTCCTCAAAAAATTCACATAGTAGAAGCTATCTGGGAAGCTAT 2100
QY 2101 TTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGA 2160
Db 2101 TTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGA 2160
QY 2161 GACTAATCTTATTCATTTTCTTAATATGCAACCATTAATAACCTTAATTTATTTAATAC 2220
Db 2161 GACTAATCTTATTCATTTTCTTAATATGCAACCATTAATAACCTTAATTTATTTAATAC 2220
QY 2221 ATACCTAAGAAGTACATTTGTTTACCTCTATATATACCAAGCACATTTTAAAAAGTGCATTA 2280
Db 2221 ATACCTAAGAAGTACATTTGTTTACCTCTATATATACCAAGCACATTTTAAAAAGTGCATTA 2280
QY 2281 CAAATGTATCAGTACGCTCTCTTTTCCAAAGAGGAGCTGAGAGATGCAAGAAATATT 2340
Db 2281 CAAATGTATCAGTACGCTCTCTTTTCCAAAGAGGAGCTGAGAGATGCAAGAAATATT 2340
QY 2341 TGTGACAAAAAATTAAGCAATTTAGAAAACTT 2372
Db 2341 TGTGACAAAAAATTAAGCAATTTAGAAAACTT 2372

RESULT 13

ACD81543
ID ACD81543 standard; cDNA; 2372 BP.
XX AC ACD81543;
XX DT 18-SEP-2003 (first entry)
XX Human cDNA encoding secreted/transmembrane protein PRO263.
XX Human; ss; gene; secreted/transmembrane protein; PRO; tumour; cancer;
XX cytostatic.
XX Homo sapiens.
XX OS
XX PN US2003009013-A1.
XX PD 09-JAN-2003.
XX PF 01-MAY-2002; 2002US-00063519.
XX PR 30-DEC-1998; 98XR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.

PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00008867.
XX
(GETH) GENENTECH INC.
Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
WPI; 2003-447384/42.
P-PSDB; ABO33937.
New isolated antibody specifically binding a PRO polypeptide, useful for
the preparation of a medicament for treating disorders with the aberrant
expression or activity of the PRO polypeptide, such as tumor conditions
and cancer.
Disclosure; Fig 5; 223pp; English.
The invention relates to an antibody that binds to a secreted or
transmembrane protein designated PRO1446 appearing as ABO33941. The
protein is one of 84 PRO polypeptides which (along with their encoding
nucleic acids) are disclosed in the specification. The methods and
compositions of the present invention are useful for the preparation of a
medicament for the treatment of disorders associated with the aberrant
expression or activity of the PRO polypeptide, such as tumour conditions
and cancer. They can also be used to generate transgenic or knockout
animals useful in the development and screening of therapeutically useful
reagents. The PRO polypeptides and encoding nucleic acids can be used as
molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The antibodies may be used in various
CC diagnostic, competitive binding and/or immunoprecipitation assays. The
CC present sequence encodes a PRO polypeptide
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
Query Match 100.0%; Score 2372; DB 7; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCAGGGAATCCGGATGTCCTGGTTATGAAGTGAGCAGTGTGAGCTTCAACATA 60
Db 1 AGCAGGGAATCCGGATGTCCTGGTTATGAAGTGAGCAGTGTGAGCTTCAACATA 60
QY 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGC 120
Db 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGC 120
QY 121 CATCTGAGTGTTTCCCTGCTGAGGGGTAGGCACGATGCGCAGGTCTTCACCTG 180
Db 121 CATCTGAGTGTTTCCCTGCTGAGGGGTAGGCACGATGCGCAGGTCTTCACCTG 180
QY 181 GTGTTGCTTCTCAGTCTCCATCTGGACACGAGCTCTCTGTCACAGGCTCTTTGCGTGCA 240
Db 181 GTGTTGCTTCTCAGTCTCCATCTGGACACGAGCTCTCTGTCACAGGCTCTTTGCGTGCA 240

QY 241 GAAGAGCTTTCCATCCAGGTGTCATGAGAAATTTATGGGATCACCTTGTGAGCAAAAAG 300
Db 241 GAAGAGCTTTCCATCCAGGTGTCATGAGAAATTTATGGGATCACCTTGTGAGCAAAAAG 300
QY 301 GCGAACCAAGCAGCTGAATTTACAGAACTAAGAGGCTCTAGGCTGCTGGGACTAAGT 360
Db 301 GCGAACCAAGCAGCTGAATTTACAGAACTAAGAGGCTCTAGGCTGCTGGGACTAAGT 360
QY 361 TTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTAT 420
Db 361 TTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTAT 420
QY 421 GGCTGGGTGGAGATGGATTCGTGTCATCTCTAGATTTAGCCCAAAACCCCAAGTGTGGG 480
Db 421 GGCTGGGTGGAGATGGATTCGTGTCATCTCTAGATTTAGCCCAAAACCCCAAGTGTGGG 480
QY 481 AAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCGGACAGATTTGAGCCCTAT 540
Db 481 AAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCGGACAGATTTGAGCCCTAT 540
QY 541 TGTACAACTCATCTGATACCTTGAACCTTAACCTGTCATTTCCAGAAATTTATCACCACCAA 600
Db 541 TGTACAACTCATCTGATACCTTGAACCTTAACCTGTCATTTCCAGAAATTTATCACCACCAA 600
QY 601 GATCCCATATTCAACACTCAAACTGCAACACAAACACAGAAATTTATTTGTCAGTGACAGT 660
Db 601 GATCCCATATTCAACACTCAAACTGCAACACAAACACAGAAATTTATTTGTCAGTGACAGT 660
QY 661 ACCTACTCGGTGGATCCCTTACTCTACAACTACCTGCCCCCTACTACTCTCTCTCTCT 720
Db 661 ACCTACTCGGTGGATCCCTTACTCTACAACTACCTGCCCCCTACTACTCTCTCTCTCT 720
QY 721 CCAGCTTCCACTTCTATTTCCAGGAGAAAATTTGATTTGTCACAGAAATTTTATG 780
Db 721 CCAGCTTCCACTTCTATTTCCAGGAGAAAATTTGATTTGTCACAGAAATTTTATG 780
QY 781 GAAACTAGCACCATGCTACAGAAACTGAACCATTTGTTGAAAATAAAAGCAGCATTTCAAG 840
Db 781 GAAACTAGCACCATGCTACAGAAACTGAACCATTTGTTGAAAATAAAAGCAGCATTTCAAG 840
QY 841 AATGAAGCTGCTGGGTGGAGGTGTCGCCAGGCTCTGCTAGTGTCTCTCTCTCTCTCT 900
Db 841 AATGAAGCTGCTGGGTGGAGGTGTCGCCAGGCTCTGCTAGTGTCTCTCTCTCTCTCT 900
QY 901 TTTGCTGCTGCACTGGTCTGGATTTGCTATGTCTATGTCAAAAGGTATGTGAAGGCTTCCCT 960
Db 901 TTTGCTGCTGCACTGGTCTGGATTTGCTATGTCTATGTCTATGTCAAAAGGTATGTGAAGGCTTCCCT 960
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Db 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAAAGAACTGATPAAAAACCCAGAAAGTCC 1080
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Db 1081 AAGAGTCCAGCAAACTACCTGCGATGCTGCGAGCTGGAAGCTGGAAGTTTGTAGATGAGAGAA 1140
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Db 1141 TGAGGAGACACACTGAGGCTGGTTCCTTTCATGTCTCTTACCTGCCCCCAGCTGGGAA 1200
QY 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCCTTAATCTGAATCAGC 1260
Db 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCCTTAATCTGAATCAGC 1260
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Db 1321 CCTGCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGCGCTTTCTAGCCTGGCTAT 1380
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Db 1381 GTCTTAATAATATCCCACTGGAGAAAGGAGTTTTCAAAGTGCAGAGCCTTAAACATC 1440
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Db 1441 TCATCAGTATCCAGTGGTAAAAAGCCCTCTGGCTGTCTGAGGCTAGTGGTGTGAAGC 1500
QY 1501 CAAGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCTTTCTTCA 1560
Db 1501 CAAGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCTTTCTTCA 1560
QY 1561 GCTCTGAAAGAGAAACAGTATCCACCTGCATGTCTCTGAGCCCGGTAAAGACAA 1620
Db 1561 GCTCTGAAAGAGAAACAGTATCCACCTGCATGTCTCTGAGCCCGGTAAAGACAA 1620
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Db 1621 AGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
QY 1681 TCTCTGTAAGCTAAAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740
Db 1681 TCTCTGTAAGCTAAAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740
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QY 1801 CACTGTTTGAACACACACACTTACTTTTCTGCTCTCTACACCTGCTGATATTTCTCT 1860
Db 1801 CACTGTTTGAACACACACACTTACTTTTCTGCTCTCTACACCTGCTGATATTTCTCT 1860
QY 1861 AGGAATAATATCTTTTACAAAGTAAACAAAATAAAAATCTCTTATAAATTTCTATTTATCT 1920
Db 1861 AGGAATAATATCTTTTACAAAGTAAACAAAATAAAAATCTCTTATAAATTTCTATTTATCT 1920
QY 1921 GAGTTTACAGAAATGATTTACTAAGGAGATTTACTCAGTAATTTGTTTAAAAAGTAAATA 1980
Db 1921 GAGTTTACAGAAATGATTTACTAAGGAGATTTACTCAGTAATTTGTTTAAAAAGTAAATA 1980
QY 1981 TTTCAACAAACATTTGCTGAAATAGCTATATGTCAAGTGTGTCGAAAGTATTACATC 2040
Db 1981 TTTCAACAAACATTTGCTGAAATAGCTATATGTCAAGTGTGTCGAAAGTATTACATC 2040
QY 2041 TGTAAATGAATATTTCTCTGAAATAGCTATATGTCAAGTGTGTCGAAAGTATTACATC 2100
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QY 2101 TTTTTCAGTTTGTATATTTCTAGCTTATCTTCCAACTAAATTTTATTTTGTGCTGA 2160
Db 2101 TTTTTCAGTTTGTATATTTCTAGCTTATCTTCCAACTAAATTTTATTTTGTGCTGA 2160
QY 2161 GACTAATCTTATTTCTCTAATATGGCAACCAATTAACCTTAATTTATTTATTAAC 2220
Db 2161 GACTAATCTTATTTCTCTAATATGGCAACCAATTAACCTTAATTTATTTATTAAC 2220
QY 2221 ATACCTAAGAGTACATTTGTTTACCTCTATATACAAAGACATTTTAAAGTGCATTA 2280
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QY 2281 CAATATGTATCACTAGCCCTCTTTTCCAAAGAGGAGCTGAGAGATGCAGAAATAT 2340
Db 2281 CAATATGTATCACTAGCCCTCTTTTCCAAAGAGGAGCTGAGAGATGCAGAAATAT 2340
QY 2341 TGTGCAAAAAAATTAAGCAITTTAGAAAACTT 2372
Db 2341 TGTGCAAAAAAATTAAGCAITTTAGAAAACTT 2372

PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-SEP-1999; 98WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00663350.
 XX

(GETH) GENENTECH INC.

XX Ashkenazi A, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini IU;
 PI Mather JF, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX WPI; 2003-147434/14.
 DR P-PSDB; ABUS4382.
 XX
 PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing or
 PT treating inflammatory diseases, organ failure, atherosclerosis, cardiac
 PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
 PT disease.
 XX
 PS Claim 2; Fig 73; 473pp; English.

XX The invention relates to an isolated PRO polypeptide having at least 80%
 CC amino acid sequence identity to: (a) any one of 61 fully defined amino
 CC acid sequences given in the specification (appearing as ABUS4347-
 CC ABUS4407); (b) an amino acid sequence encoded by the nucleotide sequence
 CC deposited under American Type Culture Collection (accession numbers
 CC listed in the specification); (c) any one of the PRO sequences which
 CC lacks its associated signal peptide; (d) an extracellular domain of the
 CC PRO polypeptide with its associated signal peptide; or (e) an
 CC extracellular domain of the PRO polypeptide which lacks its associated
 CC signal peptide. Also include are the nucleic acids encoding the PRO
 CC polypeptides, vectors, host cells and anti-PRO antibodies. The PRO
 CC polypeptides and nucleic acids are useful in diagnosing or treating
 CC enterocolitis, gastrointestinal ulceration, skin diseases associated with
 CC abnormal keratinocyte differentiation, e.g. psoriasis or epithelial
 CC cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's

CC disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g.
 CC rheumatoid arthritis, asthma or multiple sclerosis, organ failure,
 CC atherosclerosis, cardiac injury, infertility, birth defects, premature
 CC aging, AIDS, cancer, diabetic complications, or mutations in general. The
 CC polypeptides are also useful for wound repair and associated therapies
 CC concerned with re-growth of tissue. The nucleotide sequences may be used
 CC as hybridisation probes in chromosome and gene mapping, or in generating
 CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
 CC polypeptides, in assays to identify other proteins or molecules involved
 CC in binding reaction, to generate transgenic animals or knockout animals,
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, for chromosome identification, and
 CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
 CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The anti-PRO antibodies may be used in
 CC diagnostic assays for PRO, or for the affinity purification of PRO from
 CC recombinant cell culture or natural sources. The present sequence encodes
 CC a PRO polypeptide
 XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 7; Length 2372;
 Best Local Similarity 100.0%; Pred. NO. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCAGGGAATCCGATGTCGCGTTATGAGTGGAGCAGTGTGAGCCCTCAACATA 60
 Db 1 AGCAGGGAATCCGATGTCGCGTTATGAGTGGAGCAGTGTGAGCCCTCAACATA 60
 QY 61 GTTCCAGAACTCCCATCCGACTAGTTATTGAGCATCTGCTCTCATATCACAGTGGC 120
 Db 61 GTTCCAGAACTCCCATCCGACTAGTTATTGAGCATCTGCTCTCATATCACAGTGGC 120
 QY 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTGGAGCAGTGTGAGCCCTCAACATA 180
 Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTGGAGCAGTGTGAGCCCTCAACATA 180
 QY 181 GTGTTGCTTCTCACTCCATCTGAGCAGCAGAGGCTCTGTTCCAGGCTCTTTCGGTGA 240
 Db 181 GTGTTGCTTCTCACTCCATCTGAGCAGCAGAGGCTCTGTTCCAGGCTCTTTCGGTGA 240
 QY 241 GAAGAGCTTTCATCCAGGTGTCATGAGAAATATGGGATGATCCCTTTGAGCAAAAAG 300
 Db 241 GAAGAGCTTTCATCCAGGTGTCATGAGAAATATGGGATGATCCCTTTGAGCAAAAAG 300
 QY 301 GCGAACCCAGCAGCTGAATTTACAGAGAGCTTAAGGAGCCCTGTAGGCTGTGGGACTAAGT 360
 Db 301 GCGAACCCAGCAGCTGAATTTACAGAGAGCTTAAGGAGCCCTGTAGGCTGTGGGACTAAGT 360
 QY 361 TTGCGCGGCAAGCAGCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAACTTGCAGCTAT 420
 Db 361 TTGCGCGGCAAGCAGCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAACTTGCAGCTAT 420
 QY 421 GCGTGGGTTGGAGATGGAATTCGTTGCTCATCTAGGATAGCCCAACACCCCAAGTGGG 480
 Db 421 GCGTGGGTTGGAGATGGAATTCGTTGCTCATCTAGGATAGCCCAACACCCCAAGTGGG 480
 QY 481 AAAAAATGGGTTGGGTTGCTGATTTGAAAGGTTCCAGTGGAGCCGACAGTTTGCAGCTAT 540
 Db 481 AAAAAATGGGTTGGGTTGCTGATTTGAAAGGTTCCAGTGGAGCCGACAGTTTGCAGCTAT 540
 QY 541 TGTTCACACTCATCTGATATCTGAGTAACTCTGATCTCCAGAAATATACACCAAAA 600
 Db 541 TGTTCACACTCATCTGATATCTGAGTAACTCTGATCTCCAGAAATATACACCAAAA 600
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 Db 601 GATCCCATATTTCAACTCAAACTCAAACTCAAACTCAAACTCAAACTCAAACTCAAACT 660
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QY 721 CCAGCTTCCACTCTCTATTCCAGGAGAAAAAATGATTGTGTACAGAAAGTTTTATG 780
DB 721 CCAGCTTCCACTCTCTATTCCAGGAGAAAAAATGATTGTGTGTACAGAAAGTTTTATG 780
QY 781 GAACTAGACCATCTCTACAGAACTGAAACCATTTGTTGAAATTAAGCAGCATTTCAAG 840
DB 781 GAACTAGACCATCTCTACAGAACTGAAACCATTTGTTGAAATTAAGCAGCATTTCAAG 840
QY 841 AATGAAGCTGTGGGTTTTGGAGTGTCCCGAGGCTCTGCTAGTGTCTTCTCTCTCTTC 900
DB 841 AATGAAGCTGTGGGTTTTGGAGTGTCCCGAGGCTCTGCTAGTGTCTTCTCTCTCTTC 900
QY 901 TTTGGTGTCTGAGCTGGTCTTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGCCCTTCCT 960
DB 901 TTTGGTGTCTGAGCTGGTCTTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGCCCTTCCT 960
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QY 1021 GCCAATGATAGCAACCCCTAAATGAGGAATCAAAAGAAACTGTATAAAACCCAGAAAGTCC 1080
DB 1021 GCCAATGATAGCAACCCCTAAATGAGGAATCAAAAGAAACTGTATAAAACCCAGAAAGTCC 1080
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QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCTTATTGTAAC 1320
DB 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCTTATTGTAAC 1320
QY 1321 CCTGTCTGATCTTATCTCTTACCTCCAAAGCTTCCACGCTTCTAGCTGGCTAT 1380
DB 1321 CCTGTCTGATCTTATCTCTTACCTCCAAAGCTTCCACGCTTCTAGCTGGCTAT 1380
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DB 1441 TCATCAGTATCCAGTGGTAAAAAGCCCTCTGGCTGTCTGAGGCTAGTGGGTTGAAAGC 1500
QY 1501 CAAGAGTTCATGAGACCAAGGCTTCTTACTGATTCGGAGCTCAGACCCCTTCTTCA 1560
DB 1501 CAAGAGTTCATGAGACCAAGGCTTCTTACTGATTCGGAGCTCAGACCCCTTCTTCA 1560
QY 1561 GCTCTGAAAGAGAAACACATATCCACCTGACATGTCTTCTGAGCCGGTAAAGCAAA 1620
DB 1561 GCTCTGAAAGAGAAACACATATCCACCTGACATGTCTTCTGAGCCGGTAAAGCAAA 1620
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DB 1681 TCTCTGTAAGCTAAATTAAGAAATAGAACAGGCTGAGATAGCAGTACACTGTCA 1740
QY 1741 GCAGGAGCTGTAAACACAGACAGGGTCAAAGTGTCTTCTGAAACACATTTGAGTTGGAAT 1800
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DB 1801 CACTGTTTAGAACAACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
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DB 1921 GAGTTACAGAAATGANTTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
QY 1981 TTTCAAAACAAATTTGCTGAAATAGCTACTATATGTCAAGTGTCTGCAAGGTATTTACCTC 2040
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DB 2041 TGTAAATCAATATTTCTCTCAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100
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QY 2341 TGTGCAAAAAAATTAAGCAATTTAGAAAACCTT 2372
DB 2341 TGTGCAAAAAAATTAAGCAATTTAGAAAACCTT 2372

Search completed: August 18, 2004, 19:19:42

Job time : 920 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 12:05:52 ; Search time 6080 seconds

(without alignments)
11650.180 Million cell updates/sec

Title: US-10-063-670-5

Perfect score: 2372

Sequence: 1 agcagggaatcggatgc.....ttaagcatttagaaaactt 2372

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estnu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_hic:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_hic:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pln:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_nam:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrl:*
 - 28: gb_gss1:*
 - 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	1053.4	44.4	1143	9	AL574194
2	1043.8	44.0	1154	9	AL550279
3	1005.6	42.4	1201	9	AL541927
4	991.6	41.8	1201	9	AL550621

C 5	976.6	41.2	1201	13	BX397211	BX397211 BX397211
C 6	970.4	40.9	1201	9	AL547901	AL547901 AL547901
C 7	954.6	40.2	1073	9	AL552625	AL552625 AL552625
C 8	954.4	40.2	1201	9	AL546590	AL546590 AL546590
C 9	943.8	39.8	1015	9	AL552299	AL552299 AL552299
C 10	937.8	39.5	1157	9	AL575514	AL575514 AL575514
C 11	936	39.5	1201	13	BX366718	BX366718 BX366718
C 12	933	39.3	1007	9	AL575633	AL575633 AL575633
C 13	932.6	39.3	1201	9	AL574436	AL574436 AL574436
C 14	925.8	39.0	1201	9	AL546669	AL546669 AL546669
C 15	917.6	38.7	1201	9	AL541926	AL541926 AL541926
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C 27	877.2	37.0	1201	9	AL551020	AL551020 AL551020
C 28	876.2	36.9	1067	9	AL552737	AL552737 AL552737
C 29	873.2	36.8	975	9	AL576740	AL576740 AL576740
C 30	872.8	36.8	1014	9	AL553858	AL553858 AL553858
C 31	870.4	36.7	1151	9	AL550829	AL550829 AL550829
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C 38	850.4	35.9	972	9	AL549512	AL549512 AL549512
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C 40	838	35.3	911	9	AL543874	AL543874 AL543874
C 41	837	35.3	1201	13	BX334897	BX334897 BX334897
C 42	834.8	35.2	913	13	BX459046	BX459046 BX459046
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C 44	826.8	34.9	1201	13	BX366589	BX366589 BX366589
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ALIGNMENTS

RESULT 1
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LOCUS AL574194 1143 bp mRNA linear EST 31-MAY-2003
DEFINITION AL574194 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI039YJ06 3-PRIME, mRNA sequence.
ACCESSION AL574194
VERSION AL574194.2 GI:31295529
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1143)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:12934166.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI039DE03NP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI039DE03NP1.

FEATURES

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/notes="First strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

Query Match	44.4%	Score 1053.4;	DB 9;	Length 1143;
Best Local Similarity	97.3%	Pred. No. 2.5e-212;		
Matches 1083;	Conservative	8;	Mismatches 20;	Indels 2;
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bh 1143 GAGCAAAAAAATTCAGATTTKTKTCCAGAG-TTTTTTGRAAACTAGCACCATTCTTCAGAAA 1085

QY 806 CTGAACCAATTGTTGAAAAATAAAGCAGCAATTCAGATGAAGCTGCTGGGTTTGAGGTG 865

ph 1094 ACTGAACCAATTTCTGTGAAAAATAAAGCAGCAATTCAGATGAAGCTGCTGGGTTTGAGGTG 1026

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Qy	926	TTTGTCTATGTC	CAAAAGGATATG	TGTAAGGCGCTT	CCCTTTTACAAAC	CAAGAAATCAGCAG	AGG	985
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Qy	985	905	846
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CCAAAGCTAGT	CCAAAGCTAGT	CCAAAGCTAGT	CCAAAGCTAGT
TAAAGGAGGAG	TAAAGGAGGAG	TAAAGGAGGAG	TAAAGGAGGAG
GCGCAATGAT	GCGCAATGAT	GCGCAATGAT	GCGCAATGAT
AGCAACCTTA	AGCAACCTTA	AGCAACCTTA	AGCAACCTTA
TATGAGG	TATGAGG	TATGAGG	TATGAGG

QY	1045	AATCAAGAGAAACTGATATAAACCCAGAGAGTCCAGAGTCCAGAGCAAACTACCGTGC	1105
DB	845	AATCAAGAGAAACTGATATAAACCCAGAGAGAGTCCAGAGTCCAGAGCAAACTACCGTGC	786

Accession	Sequence	Length
Qy	GATGCCTGAAAGCTGAAGTTTTCAGTACAGACAGAATGAGGAGACACACCTGAGCTGGTT	1166
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Accession	Sequence	Length
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QY 1346 TCCAAAGCTTCCCAAGCGGCTTTCTAGCCCTGGCTATGTCCTAATAATATCCCACTGGGAGA 486

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QY
1406 AAGGAAATTTCTCAAAAATTCTCATCAGTATCCAGTGGTAAAAAGG 426

Dd
485 AAGGAGTTTTGCAAGTCGAAGACCTAAACAATCTCATCAGTATCCAGTGGTAAAAAGG 426

425 CCTCTGGCTGCTCTGAGGCTAGGTGGGTTGAAAGCCAGGAGTCACTGAGACCGAGGCTT 365

365	TCTCTACTGATTCGGAGCTCAGACCCCTTTCTTCAGCTCTGAAGAGAAACACGCTATCCC	306
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305	KCTTCACATGTCTTCTGAGCCCGGTAAAGAGCAAAAGATGGKGDARRGTTTAGCCCK	246
1646	GAAGCCATGGAGATTCTATACTTGAGACCTTAATCTGTGTAAGCTAAATAAGAAA	1705
245	GAAGCCATGGAGATTCTATACTTGAGACCTTAATCTGTGTAAGCTAAATAAGAAA	186
1706	TAGAACCAAGCTGAGGATACGACAGTACACTGTGACAGGACCTGTAAACACACACAGG	1765
185	TAGAACCAAGCTGAGGATACGACAGTACACTGTGACAGGACCTGTAAACACACACAGG	126
1766	TCAAGTGTTTTCTCTGAACACATTGAGTTGGAACTCACTTTTAGACACACACACTTAC	1825
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1826	TTTTTCTGGTCTCAACCAGCTGCTGATATTTCT	1858
65	TTTTTCTGGTCTCAACCAGCTGCTGATATTTCT	33

[illegible]

ncup://www.genoscope.cns.1237
cgi-bin/cluster.cgi?seq=CS0DF039DE03QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DF039DE03QP1.

FEATURES	source
rainbow	Location/Qualifiers
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ORIGIN

Query Match	44.0%;	Score 1043.8;	DB 9;	Length 1154;
Best Local Similarity	98.9%;	Pred. NO. 2.7e-210;		
Matches 1057.	Conservative	4: Mismatches 6;	Indels 2;	Gaps 1

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QY 162 GGCAGGTCCTCAGCTGGTGTGCTTCTCACTTCATCTGACACACAGAGGCTCTGGT 221
Db 124 GGCAGGTCCTCAGCTGGTGTGCTTCTCACTTCATCTGACACACAGAGGCTCTGGT 183
QY 222 CCAAGGCTCTTTCGCTGCAGAGAGCTTTTCATCCAGGTGTCTATGCAGAAATATGGGAT 281
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QY 282 CACCTCTGTGAGCAAAAAGCCGACACAGAGCTGAATTTACAGAAAGTCAAGAGGCTCG 341
Db 244 CACCTCTGTGAGCAAAAAGCCGACACAGAGCTGAATTTACAGAAAGTCAAGAGGCTCG 303
QY 342 TAGGCTGCTGGACTAAGTTTGGCCGGCAGGACCAAGTTGAACAGCTTGAACCTAG 401
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QY 402 CTTTGAATCTTGAGCTATGGCTGGGTGGAGATGATTCGTGCTCATCTCTAGGATTAG 461
Db 364 CTTTGAATCTTGAGCTATGGCTGGGTGGAGATGATTCGTGCTCATCTCTAGGATTAG 423
QY 462 CCAAAACCCCAAGTGTGGAAAAAATGGGTGGGTGCTCTGATTTGAAGGTTCCAGTGAG 521
Db 424 CCAAAACCCCAAGTGTGGAAAAAATGGGTGGGTGCTCTGATTTGAAGGTTCCAGTGAG 483
QY 522 CGCAGATTTGAGCTATGTTGTAACCTCACTGATCTGATCTGAGCTAATCTGTCGATTC 581
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QY 762 TGTCACAGAAAGTTTATGGAACCTAGCAACCTATGTCACAGAACTGAACCACTTTGTCGA 821
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Db 904 GTATGTGAAGGCT 963
QY 1002 AGTAGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1061
Db 964 AGTAGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1023
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LOCUS AL541927 1201 bp mRNA linear EST 12-MAY-2003
DEFINITION AL541927 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE007YF17
5-PRIME, mRNA sequence.
ACCESSION AL541927
VERSION AL541927.2 GI:30546572
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12873466.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE007CC090P1&cluster=5952.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE007CC090P1.
Location/Qualifiers
1..1201
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

FEATURES
source

ORIGIN

Query Match 42.4%; Score 1005.6; DB 9; Length 1201;
Best Local Similarity 95.5%; Pred. No. 3.2e-202;
Matches 1060; Conservative 15; Mismatches 29; Indels 6; Gaps 4;
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Db 235 CTCATCAGTATCCAGTGGTAAAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 294
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Db 295 CCAAGGAGTCACTGAGACCAAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 354
QY 1560 AGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1619
Db 355 AGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 414
QY 1620 AAGAAATGGCAAAAAGTTTAGCCCTCTGAAAGCCATGGAGATTTCTCATTAACCTT 1679
Db 415 AAGAAATGGCAAAAAGTTTAGCCCTCTGAAAGCCATGGAGATTTCTCATTAACCTT 474

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1201)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:12882399.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5952.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1033CB06NP1&cluster=5952.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D1033CB06NP1.
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 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
 source

ORIGIN

Query Match 40.9%; Score 970.4; DB 9; Length 1201;
 Best Local Similarity 98.6%; Pred. No. 9e-195;
 Matches 986; Conservative 7; Mismatches 5; Indels 2; Gaps 2;

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 1698 TAAAGAAATAGAACAAAGCTGAGGATACGACATGCTGAGCAGGAGCTGTAACAC 1757
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478 AAGTAACAAAAATAAAACTCTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATT 419
 1938 ACTAAGGAAGATTTACTCAGTAATTTGTTTAAAAGTAAATAAAATCAACAAACATTTGCT 1997
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 clone CS0D1067Y15 3-PRIME, mRNA sequence.
 ACCESSION AL552625
 VERSION AL552625.2 GI:31274440
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1073)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:12891706.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5952.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1067AD08NP1&cluster=5952.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
 source

or

QY	1104	789	Db
	GCATGCTCGAAGCTGAAGTTTAGATGACACAGAAATGAGGAGACACACTGAGCTGG	CGCATGCTCGAAGCTGAAGTTTAGATGACAGAAATGAGGAGACACACCGAGCTGG	730

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Db 669 GAAGAAAGTCCACCTTGGTTCCTAACCTGAATCAGCTCAGGACTGCGCATTTGGACTATGG 610
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QY 1344 CCTCAAAGCTTCCACCGGCTTTCTAGCCTGGCTATGCTCTTAATAATATCCCACTGGGA 1403
Db 549 CCTCAAAGCTTCCACCGGCTTTCTAGCCTGGCTATGCTCTTAATAATATCCCACTGGGA 490
QY 1404 GAAAGAGTTTTCAGAGTGAAGAGCTTAAACATCTCATCAGTATCCAGTGTTAAAAA 1463
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QY 1464 GGCTCTCTGGCTGCTGAGGCTAGTGGTTGAAAGCCAGGAGTCACTGAGACCAAGGC 1523
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QY 1764 GGTCAAAGTGTTCCTGGAACATATTGAGTTGGAATCAGTGTAGAACACACACACTT 1823
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LOCUS AL552299
DEFINITION AL552299 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1069YN02 5-PRIME, mRNA sequence.
ACCESSION AL552299
VERSION AL552299.2 GI:31274114
KEYWORDS EST.
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1015)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12891068.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
```

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
<http://www.genoscope.cns.fr/>
cgi-bin/cluster.cgi?seq=CS0D1069DG01QPI&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0D1069DG01QPI.

FEATURES

source

1..1015
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0D1069YN02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="First strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the NotI and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 39.8%; Score 943.8; DB 9; Length 1015;
Best Local Similarity 99.8%; Pred. No. 3.9e-189;
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 78 CCGGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCC 137
Db 62 CGGATGATTGTTATTGAGCATCTGCTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCC 121
QY 138 TGGCTCTGAAGGGGTAGGACGATGGCAGGTGTTTTCAGCTGGTGTGTTTCTCATCTTC 197
Db 122 TGGCTCTGAAGGGGTAGGACGATGGCAGGTGTTTTCAGCTGGTGTGTTTCTCATCTTC 181
QY 198 CATCTGACACGAGGCTCTGTTCCAGGCTCTTTGGTGCAGAGAGCTTTCCATCCA 257
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QY 258 GGTCTGATGACAGATTATTGGGATCACCCCTTGTGAGCAAAAAGCGAACACAGAGCTGAA 317
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QY 318 TTTCACAGAACTAAGGAGGCTGTAGCTCTCTGGACTTAAGTTGGCCGCAAGACCA 377
Db 302 TTTCACAGAACTAAGGAGGCTGTAGCTCTCTGGACTTAAGTTGGCCGCAAGACCA 361
QY 378 AGTTGAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGG 437
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QY 438 ATTCTGTGCTATCTTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAATGGGTGGTGT 497
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Best Local Similarity 96.4%; Pred. No. 7.5e-187;
Matches 974; Conservative 19; Mismatches 12; Indels 5; Gaps 4;

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DB 1007 GCTCTCCTCTCTTT--GTGCTGCAGCTG--TCTTGGATTGGCTATGTCATAAGGTATGTG 951

QY 949 AAGGCTTTCCCTTTTACAAACAGAAATCAGCAGAAAGAAATGATCGAAACCAAGTAGTA 1008
DB 950 AAGGCTTTCCCTTTTACAAACAGAAATCAGCAGAAAGAAATGATCGAAACCAAGTAGTA 891

QY 1009 AAGGAGAGAGAGCCCAATGATACCAACCTTAATGAGGAATCAAGAAACCTGATATAAAAC 1068
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QY 1069 CCAGAGAGTCCAGAGTCCAGCAAAACTACCGTGCATGCCCTGGAAGCTGAAGTTTAG 1128
DB 830 CCAGAGAGTCCAGAGTCCAGCAAAACTACCGTGCATGCCCTGGAAGCTGAAGTTTAG 771

QY 1129 ATGAGACAGAAATGAGAGACACACCTGAGGCTGGTTTCTTTCATGCTCTTACCTGCC 1188
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QY 1189 CCAGCTGGGGAAATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTTGTTCCCTA 1248
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QY 1309 CTTTATTTGAACCTGTCTGGATCTTATCTCTACTCTCAAGAGCTTCCACGSCCTTTC 1368
DB 590 CTTTATTTGAACCTGTCTGGATCTTATCTCTACTCTCAAGAGCTTCCACGSCCTTTC 531

QY 1369 TAGCCTGGCTATGCTCTTAATATATCCACTGGGAGAAAGAGTTTGGAAAGTCAAGG 1428
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QY 1728 CAGTACACTGTGAGAGGACTGTAAACACAGACAGGGTCAAGTGTCTTCTCTGAGCAC 1787
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QY 1788 ATTGAGTTGGAATCACTGTTTAGAACACACACACTTTTCTGGTCTCTA-CCACTG 1846
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QY 1847 CTGATATTTTCTAGGAAATATACCTTTTACAGTAAACAAAATAAAAC 1896
DB 50 CTGATATTTTNTATAGAAAATATATTTTACAAATAGNNAWHWTABADC 1
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DEFINITION
1201 bp mRNA linear EST 01-JUN-2003
clone CS0DI058YN14 3-PRIME, mRNA sequence.
ACCESSION
AL574436
VERSION
AL574436.2 GI:31312754
KEYWORDS
EST.
SOURCE
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ORGANISM
Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12934641.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
c91-bin/cluster.cgi?seq=CS0DI058DG07NP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DI058DG07NP1.
Location/Qualifiers
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match      39.3%; Score 932.6; DB 9; Length 1201;
Best Local Similarity 95.7%; Pred. No. 9e-187;
Matches 979; Conservative 16; Mismatches 23; Indels 5; Gaps 4;

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DB 1024 YCTCTTCTCCAAAGCTTCCCMC-GCCTTCTAGCTTGTCTATGTCCT-ATWATAYCCC 967

QY 1397 ACTGGAGAGAGAGTGTTCAAAGTGCAAGGACCTTAAACATCTCATCAGTATCCAGTG 1456
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QY 1457 GTAAAAAGGCTCTCGGCTGTCTGAGGCTAGTGGTGTGAAAGCCAAAGAGTACTGAGA 1516
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DB 846 CCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCTTCTTCTCAGTCTGGAAGAGAAC 787

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DB 786 AGCTATCCCACTGACATGTCTTCTGAGCCCGGTAAAGCAAAAGATGGCAGAAAAGT 727

QY 1637 TTAGCCCTGAAAGCCATGGAGTCTCATAACTTTGAGACCTTAATCTCTGTAAGCTAAA 1696
DB 726 TTAGCCCTGAAAGCCATGGAGTCTCATAACTTTGAGACCTTAATCTCTGTAAGCTAAA 667

QY 1697 ATAAAGAAATAGAACAAAGCTGAGATAGCAGTACACTGTGACAGGACTGTAAACA 1756
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DEFINITION clone CS0D1029YJ09 5-PRIME, mRNA sequence.
ACCESSION AL546669
VERSION AL546669.2 GI:31268502
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12880008.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
```

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cgi-bin/cluster.cgi?seq=CS0D1029CE05QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0D1029CE05QP1.
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/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 39.0%; Score 925.8; DB 9; Length 1201;
Best Local Similarity 95.3%; Pred. No. 2.5e-185;
Matches 983; Conservative 4; Mismatches 36; Indels 8; Gaps 3;
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Qy 145 GAAGGGGTAGGCAGATGGCCAGGTGCTTCAAGCTGTGTTGCTTCTCAGTTCATCTGG 204
Db 111 GAAGGGGTAGGCAGATGGCCAGGTGCTTCAAGCTGTGTTGCTTCTCAGTTCATCTGG 170
Qy 205 ACCACGAGGTCTGTGTCCTCAAGGCTCTTGGCTGCAGAGGCTTCCATCCAGTGTCA 264
Db 171 ACCACGAGGTCTGTGTCCTCAAGGCTCTTGGCTGCAGAGGCTTCCATCCAGTGTCA 230
Qy 265 TGCAGATATTGGGGATCCCTTCTGAGCAAAAGGCGACCGACGCTGAATTTTACA 324
Db 231 TGCAGATATTGGGGATCCCTTCTGAGCAAAAGGCGACCGACGCTGAATTTTACA 290
Qy 325 GAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAA 384
Db 291 GAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAA 350
Qy 385 ACAGCTTGAAGCTAGCTTTGAACTTGCAGCTATGCTGGTGGTGGAGATGGATTCGTG 444
Db 351 ACAGCTTGAAGCTAGCTTTGAACTTGCAGCTATGCTGGTGGTGGAGATGGATTCGTG 410
Qy 445 GTCATCTAGGATTAGCCCAACCCCAAGTGTGGGAAAATGGGTGGGTGCTCTGATT 504
Db 411 GTCATCTAGGATTAGCCCAACCCCAAGTGTGGGAAAATGGGTGGGTGCTCTGATT 470
Qy 505 TGGAGGTTCCAGTGAGCCGACAGTTTGCAGCTTATTTTCAACTCATCTGATCTTGG 564
Db 471 TGGAGGTTCCAGTGAGCCGACAGTTTGCAGCTTATTTTCAACTCATCTGATCTTGG 530
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Db 531 ACTAATCTGTCATTCGAAATTTATACCAACCAAGATCCCATTTTCAACACTCAAACT 590
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Job time : 6086 secs

OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 22:49:08 ; Search time 1034 Seconds
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11255.777 Million cell updates/sec

Title: US-10-063-670-5

Perfect score: 2372

Sequence: 1 agcagggaataccggtatgc.....ttaagcatttagaagaactt 2372

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues 6451454

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 800 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2372	100.0	2372	9	US-09-902-853-200
5	2372	100.0	2372	9	US-09-907-824-200
6	2372	100.0	2372	9	US-09-907-841-200
7	2372	100.0	2372	10	US-09-904-011-200
8	2372	100.0	2372	10	US-09-906-742-200
9	2372	100.0	2372	10	US-09-906-838-200
10	2372	100.0	2372	10	US-09-907-613-200
11	2372	100.0	2372	10	US-09-907-942-200
12	2372	100.0	2372	10	US-09-904-859-200
13	2372	100.0	2372	10	US-09-909-204-200
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16	2372	100.0	2372	10	US-09-909-088B-200
17	2372	100.0	2372	10	US-09-905-291A-200
18	2372	100.0	2372	10	US-09-902-853-200
19	2372	100.0	2372	10	US-09-907-824-200
20	2372	100.0	2372	10	US-09-907-841-200
21	2372	100.0	2372	10	US-09-904-011-200
22	2372	100.0	2372	10	US-09-906-742-200
23	2372	100.0	2372	10	US-09-906-838-200
24	2372	100.0	2372	10	US-09-907-613-200
25	2372	100.0	2372	10	US-09-907-942-200
26	2372	100.0	2372	10	US-09-904-859-200
27	2372	100.0	2372	10	US-09-909-204-200
28	2372	100.0	2372	10	US-09-909-320-200
29	2372	100.0	2372	10	US-09-909-088B-200
30	2372	100.0	2372	10	US-09-905-291A-200
31	2372	100.0	2372	10	US-09-902-853-200
32	2372	100.0	2372	10	US-09-907-824-200
33	2372	100.0	2372	10	US-09-907-841-200
34	2372	100.0	2372	10	US-09-904-011-200
35	2372	100.0	2372	10	US-09-906-742-200
36	2372	100.0	2372	10	US-09-906-838-200
37	2372	100.0	2372	10	US-09-907-613-200
38	2372	100.0	2372	10	US-09-907-942-200
39	2372	100.0	2372	10	US-09-904-859-200
40	2372	100.0	2372	10	US-09-909-204-200
41	2372	100.0	2372	10	US-09-909-320-200
42	2372	100.0	2372	10	US-09-909-088B-200
43	2372	100.0	2372	10	US-09-905-291A

234	2372	100.0	2372	16	US-10-449-656-200	Sequence 200, App	307	53.2	2.2	622	13	US-10-424-599-3380	Sequence 3380, App
235	2372	100.0	2372	16	US-10-448-713-200	Sequence 200, App	C 308	53	2.2	6544	15	US-10-239-676-45	Sequence 45, Appl
236	2372	100.0	2372	17	US-10-425-447-200	Sequence 200, App	C 309	53	2.2	6544	15	US-10-311-455-619	Sequence 619, App
237	2372	100.0	2372	17	US-10-215-371-200	Sequence 200, App	C 310	53	2.2	8101	15	US-10-311-455-1952	Sequence 1952, App
238	2372	100.0	2404	9	US-09-833-881-849	Sequence 849, App	C 311	53	2.2	13574	15	US-10-311-455-1290	Sequence 1290, App
239	2372	100.0	2404	9	US-09-833-381-853	Sequence 853, App	C 312	52.6	2.2	843	13	US-10-027-632-7034	Sequence 7034, App
240	2342.2	98.7	2369	16	US-10-464-237-1260	Sequence 1260, App	C 313	52.6	2.2	843	13	US-10-027-632-7034	Sequence 7034, App
241	2313.2	97.5	2324	13	US-10-276-774-999	Sequence 999, App	C 314	52.4	2.2	3252	13	US-10-027-632-113786	Sequence 113786, App
242	2290.2	96.6	2313	15	US-10-291-634-1	Sequence 1, Appl	C 315	52.4	2.2	3252	13	US-10-027-632-113787	Sequence 113787, App
243	1994	84.1	2029	15	US-10-079-111-2	Sequence 2, Appl	C 316	52.4	2.2	3252	16	US-10-027-632-113786	Sequence 113786, App
244	967.4	40.8	1127	16	US-10-138-588-1	Sequence 595, App	C 317	52.4	2.2	3252	16	US-10-027-632-113787	Sequence 113787, App
245	603.6	25.4	1896	15	US-10-152-861-595	Sequence 595, App	C 318	52.4	2.2	3252	16	US-10-027-632-113788	Sequence 113788, App
246	603.6	25.4	1896	15	US-10-152-861-595	Sequence 595, App	C 319	52.4	2.2	3252	16	US-10-027-632-113788	Sequence 113788, App
247	500.2	21.1	516	9	US-09-962-436-348	Sequence 348, App	C 320	51.8	2.2	755	13	US-10-027-632-128109	Sequence 128109, App
248	500.2	21.1	516	9	US-09-954-456-834	Sequence 834, App	C 321	51.8	2.2	755	13	US-10-027-632-128109	Sequence 128109, App
249	500.2	21.1	516	9	US-09-954-456-834	Sequence 834, App	C 322	51.8	2.2	9832	15	US-10-311-455-629	Sequence 629, App
250	500.2	21.1	516	9	US-09-880-107-114	Sequence 114, App	C 323	51.6	2.2	16750	13	US-10-221-714A-36	Sequence 36, Appl
251	500.2	21.1	516	9	US-09-954-531-633	Sequence 633, App	C 324	51.6	2.2	16750	13	US-10-221-714A-36	Sequence 36, Appl
252	500.2	21.1	516	9	US-09-954-531-633	Sequence 633, App	C 325	51.4	2.2	12337	15	US-10-311-455-494	Sequence 494, Appl
253	485.8	20.5	506	9	US-09-778-320-96	Sequence 1042, App	C 326	51	2.2	3673778	15	US-10-312-841-2	Sequence 2, Appl
254	485.8	20.5	506	9	US-09-910-689-96	Sequence 96, Appl	C 327	50.8	2.1	5407	15	US-10-433-793-104	Sequence 104, App
255	485.8	20.5	506	14	US-10-010-742-96	Sequence 96, Appl	C 328	50.6	2.1	392	9	US-10-311-455-2063	Sequence 2063, App
256	485.8	20.5	506	17	US-10-714-389-96	Sequence 96, Appl	C 329	50.6	2.1	392	9	US-09-960-352-4808	Sequence 4808, App
257	485.8	20.5	506	17	US-10-717-236-96	Sequence 96, Appl	C 330	50.4	2.1	5504	13	US-10-221-613-270	Sequence 270, App
258	440	18.5	486	10	US-09-918-995-10116	Sequence 10116, A	C 331	50	2.1	12337	15	US-10-311-455-2331	Sequence 2331, App
259	419.4	17.7	472	10	US-09-918-995-9451	Sequence 9451, App	C 332	50	2.1	50	9	US-09-909-088B-205	Sequence 205, App
260	406	17.1	441	10	US-09-918-995-4294	Sequence 4294, App	C 333	50	2.1	50	9	US-09-905-291A-205	Sequence 205, App
261	403	17.0	441	10	US-09-918-995-4294	Sequence 4294, App	C 334	50	2.1	50	9	US-09-905-291A-205	Sequence 205, App
262	397	16.7	411	10	US-09-918-995-8107	Sequence 8107, App	C 335	50	2.1	50	9	US-09-907-824-205	Sequence 205, App
263	387.6	16.3	820	15	US-10-079-111-5	Sequence 5, Appl	C 336	50	2.1	50	9	US-09-907-841-205	Sequence 205, App
264	334	14.1	339	15	US-10-291-634-11	Sequence 11, Appl	C 337	50	2.1	50	10	US-09-904-011-205	Sequence 205, App
265	328.6	13.9	559	13	US-10-079-111-3	Sequence 3, Appl	C 338	50	2.1	50	10	US-09-906-742-205	Sequence 205, App
266	318.4	13.4	334	13	US-10-085-783A-42439	Sequence 42439, A	C 339	50	2.1	50	10	US-09-906-838-205	Sequence 205, App
267	318.4	13.4	334	16	US-10-242-535A-42439	Sequence 42439, A	C 340	50	2.1	50	10	US-09-907-613-205	Sequence 205, App
268	296.8	12.5	492	15	US-10-291-634-12	Sequence 12, Appl	C 341	50	2.1	50	10	US-09-907-942-205	Sequence 205, App
269	239	10.1	241	9	US-09-604-287A-324	Sequence 324, App	C 342	50	2.1	50	10	US-09-904-859-205	Sequence 205, App
270	239	10.1	241	10	US-09-551-621-324	Sequence 324, App	C 343	50	2.1	50	10	US-09-903-204-205	Sequence 205, App
271	239	10.1	241	14	US-10-007-805-324	Sequence 324, App	C 344	50	2.1	50	10	US-09-904-820-205	Sequence 205, App
272	239	10.1	241	15	US-10-076-622-324	Sequence 324, App	C 345	50	2.1	50	10	US-09-904-786-205	Sequence 205, App
273	239	10.1	241	15	US-10-124-805-324	Sequence 324, App	C 346	50	2.1	50	10	US-09-906-646-205	Sequence 205, App
274	238	10.0	308	9	US-09-880-107-1687	Sequence 1687, App	C 347	50	2.1	50	10	US-09-906-700-205	Sequence 205, App
275	238	10.0	308	9	US-09-954-531-654	Sequence 654, App	C 348	50	2.1	50	10	US-09-903-785-205	Sequence 205, App
276	238	10.0	308	9	US-09-954-531-1067	Sequence 1067, App	C 349	50	2.1	50	10	US-09-903-903-205	Sequence 205, App
277	238	10.0	308	9	US-09-954-531-1068	Sequence 1068, App	C 350	50	2.1	50	10	US-09-903-749A-205	Sequence 205, App
278	237	10.0	241	9	US-09-604-287A-323	Sequence 323, App	C 351	50	2.1	50	10	US-09-904-119-205	Sequence 205, App
279	237	10.0	241	10	US-09-551-621-323	Sequence 323, App	C 352	50	2.1	50	10	US-09-904-956-205	Sequence 205, App
280	237	10.0	241	14	US-10-007-805-323	Sequence 323, App	C 353	50	2.1	50	10	US-09-902-736-205	Sequence 205, App
281	237	10.0	241	15	US-10-076-622-323	Sequence 323, App	C 354	50	2.1	50	10	US-09-907-794-205	Sequence 205, App
282	237	10.0	241	15	US-10-124-805-323	Sequence 323, App	C 355	50	2.1	50	10	US-09-903-943-205	Sequence 205, App
283	226.2	9.5	239	9	US-09-954-456-913	Sequence 913, App	C 356	50	2.1	50	10	US-09-904-462-205	Sequence 205, App
284	226.2	9.5	239	9	US-09-954-456-1513	Sequence 1513, App	C 357	50	2.1	50	10	US-09-907-925-205	Sequence 205, App
285	226.2	9.5	239	9	US-09-880-107-725	Sequence 725, App	C 358	50	2.1	50	10	US-09-902-692-205	Sequence 205, App
286	226.2	9.5	239	9	US-09-954-531-875	Sequence 875, App	C 359	50	2.1	50	10	US-09-903-520-205	Sequence 205, App
287	226.2	9.5	239	9	US-09-954-531-1285	Sequence 1285, App	C 360	50	2.1	50	10	US-09-905-056-205	Sequence 205, App
288	226.2	9.5	239	15	US-09-954-531-1285	Sequence 1285, App	C 361	50	2.1	50	10	US-09-909-064-205	Sequence 205, App
289	212.2	8.9	279	15	US-10-291-634-14	Sequence 14, Appl	C 362	50	2.1	50	10	US-09-904-553-205	Sequence 205, App
290	191.4	8.1	466	15	US-10-079-111-4	Sequence 4, Appl	C 363	50	2.1	50	10	US-09-905-381-205	Sequence 205, App
291	179.2	7.6	469	9	US-09-864-761-2325	Sequence 13, Appl	C 364	50	2.1	50	10	US-09-905-088-205	Sequence 205, App
292	175	7.4	457	9	US-09-864-761-15431	Sequence 15431, A	C 365	50	2.1	50	10	US-09-907-575-205	Sequence 205, App
293	160	6.7	498	15	US-10-291-634-15	Sequence 15, Appl	C 366	50	2.1	50	10	US-09-905-075-205	Sequence 205, App
294	129	5.4	141	9	US-09-864-761-19060	Sequence 19060, A	C 367	50	2.1	50	10	US-09-902-759-205	Sequence 205, App
295	106	4.5	106	9	US-09-864-761-31946	Sequence 31946, A	C 368	50	2.1	50	10	US-09-902-634-205	Sequence 205, App
296	96.8	4.1	467	16	US-10-191-803-1134	Sequence 1134, App	C 369	50	2.1	50	10	US-09-902-713-205	Sequence 205, App
297	93	3.9	836	13	US-10-027-632-148987	Sequence 148987, A	C 370	50	2.1	50	10	US-09-907-979-205	Sequence 205, App
298	93	3.9	836	16	US-10-027-632-148987	Sequence 148987, A	C 371	50	2.1	50	10	US-09-902-615-205	Sequence 205, App
299	60	2.5	641	12	US-09-908-975-10869	Sequence 10869, A	C 372	50	2.1	50	10	US-09-903-925-205	Sequence 205, App
300	58.2	2.5	641	12	US-09-969-034-389	Sequence 389, App	C 373	50	2.1	50	10	US-09-906-760A-205	Sequence 205, App
301	58	2.4	3673778	15	US-10-312-841-2	Sequence 2, Appl	C 374	50	2.1	50	10	US-09-903-823-205	Sequence 205, App
302	56.6	2.4	6216	17	US-10-257-166-13	Sequence 13, Appl	C 375	50	2.1	50	10	US-09-907-652-205	Sequence 205, App
303	55	2.3	83391	17	US-10-433-793-123	Sequence 123, App	C 376	50	2.1	50	10	US-09-902-572A-205	Sequence 205, App
304	54.2	2.3	15373	15	US-10-311-455-440	Sequence 440, App	C 377	50	2.1	50	10	US-09-902-979-205	Sequence 205, App
305	53.8	2.3	11790	15	US-10-311-455-515	Sequence 515, App	C 378	50	2.1	50	10	US-09-905-125-205	Sequence 205, App
306	53.4	2.3	3673778	15	US-10-312-841-1	Sequence 1, Appl	C 379	50	2.1	50	10	US-09-906-815A-205	Sequence 205, App

380	50	2.1	50	10	US-09-905-449-205	Sequence 205, App	453	48.2	2.0	3476	13	US-10-245-752-51	Sequence 51, Appl
381	50	2.1	50	10	US-09-903-806-205	Sequence 205, App	454	48.2	2.0	3476	13	US-10-245-859-51	Sequence 51, Appl
382	50	2.1	50	10	US-09-904-992-205	Sequence 205, App	455	48.2	2.0	3476	15	US-10-245-103-51	Sequence 51, Appl
383	50	2.1	50	10	US-09-904-838-205	Sequence 205, App	456	48.2	2.0	3476	15	US-10-245-107-51	Sequence 51, Appl
384	50	2.1	50	10	US-09-906-777-205	Sequence 205, App	457	48.2	2.0	3476	15	US-10-245-143-51	Sequence 51, Appl
385	50	2.1	50	10	US-09-903-603A-205	Sequence 205, App	458	48.2	2.0	3476	15	US-10-245-771-51	Sequence 51, Appl
386	50	2.1	50	10	US-09-904-532-205	Sequence 205, App	459	48.2	2.0	3476	15	US-10-245-851-51	Sequence 51, Appl
387	50	2.1	50	10	US-09-904-766-205	Sequence 205, App	460	48.2	2.0	3476	15	US-10-245-883-51	Sequence 51, Appl
388	50	2.1	50	10	US-09-904-920A-205	Sequence 205, App	461	48.2	2.0	3476	15	US-10-237-535-51	Sequence 51, Appl
389	50	2.1	50	10	US-09-904-877A-205	Sequence 205, App	462	48.2	2.0	3476	15	US-10-238-183-51	Sequence 51, Appl
390	50	2.1	50	10	US-09-903-562-205	Sequence 205, App	463	48.2	2.0	3476	15	US-10-238-283-51	Sequence 51, Appl
391	50	2.1	50	10	US-09-906-618-205	Sequence 205, App	464	48.2	2.0	3476	15	US-10-238-370-51	Sequence 51, Appl
392	50	2.1	50	10	US-09-907-728-205	Sequence 205, App	465	48.2	2.0	3476	15	US-10-245-055-51	Sequence 51, Appl
393	50	2.1	50	11	US-09-904-805-205	Sequence 205, App	466	48.2	2.0	3476	15	US-10-245-147-51	Sequence 51, Appl
394	50	2.1	50	11	US-09-904-938A-205	Sequence 205, App	467	48.2	2.0	3476	15	US-10-245-730-51	Sequence 51, Appl
395	50	2.1	50	11	US-09-906-722A-205	Sequence 205, App	468	48.2	2.0	3476	15	US-10-245-739-51	Sequence 51, Appl
396	50	2.1	50	11	US-09-908-576-205	Sequence 205, App	469	48.2	2.0	3476	15	US-10-246-210-51	Sequence 51, Appl
397	50	2.1	50	13	US-09-903-640-205	Sequence 205, App	470	48.2	2.0	3476	15	US-10-239-196-51	Sequence 51, Appl
398	50	2.1	50	13	US-09-908-093-205	Sequence 205, App	471	48.2	2.0	3476	15	US-10-243-024-51	Sequence 51, Appl
399	50	2.1	50	13	US-09-904-485-205	Sequence 205, App	472	48.2	2.0	3476	15	US-10-243-409-51	Sequence 51, Appl
400	50	2.1	50	13	US-09-905-348-205	Sequence 205, App	473	48.2	2.0	3476	15	US-10-245-621-51	Sequence 51, Appl
401	50	2.1	50	13	US-10-238-993-205	Sequence 205, App	474	48.2	2.0	3476	15	US-10-245-880-51	Sequence 51, Appl
402	50	2.1	50	13	US-10-448-923-205	Sequence 205, App	475	48.2	2.0	3476	15	US-10-245-033-51	Sequence 51, Appl
403	50	2.1	50	15	US-10-299-976-205	Sequence 205, App	476	48.2	2.0	3476	15	US-10-243-095-51	Sequence 51, Appl
404	50	2.1	50	15	US-10-299-976-205	Sequence 205, App	477	48.2	2.0	3476	15	US-10-245-185-51	Sequence 51, Appl
405	50	2.1	50	16	US-10-299-937-205	Sequence 205, App	478	48.2	2.0	3476	15	US-10-245-427-51	Sequence 51, Appl
406	50	2.1	50	16	US-10-449-656-205	Sequence 205, App	479	48.2	2.0	3476	15	US-10-245-770-51	Sequence 51, Appl
407	50	2.1	50	16	US-10-448-713-205	Sequence 205, App	480	48.2	2.0	3476	15	US-10-245-877-51	Sequence 51, Appl
408	50	2.1	50	17	US-10-425-447-205	Sequence 205, App	481	48.2	2.0	3476	15	US-10-246-976-51	Sequence 51, Appl
409	50	2.1	50	17	US-10-215-371-205	Sequence 205, App	482	48.2	2.0	3476	15	US-10-243-320-51	Sequence 51, Appl
410	50	2.1	37515	17	US-10-433-793-28	Sequence 205, App	483	48.2	2.0	3476	15	US-10-243-411-51	Sequence 51, Appl
411	49.4	2.1	8305	17	US-10-311-455-1542	Sequence 1542, App	484	48.2	2.0	3476	15	US-10-242-743-51	Sequence 51, Appl
412	49.4	2.1	77841	17	US-10-433-580-3	Sequence 3, Appl	485	48.2	2.0	3476	15	US-10-243-425-51	Sequence 51, Appl
413	49.4	2.1	73334	15	US-10-311-455-2098	Sequence 2098, App	486	48.2	2.0	3476	15	US-10-243-446-51	Sequence 51, Appl
414	49.2	2.1	73334	17	US-10-240-589C-128	Sequence 128, App	487	48.2	2.0	3476	15	US-10-237-636-51	Sequence 51, Appl
415	49.2	2.1	7461	15	US-10-311-455-1757	Sequence 1757, App	488	48.2	2.0	3476	15	US-10-238-325-51	Sequence 51, Appl
416	49.2	2.1	21354	13	US-10-221-7148-512	Sequence 512, App	489	48.2	2.0	3476	15	US-10-238-346-51	Sequence 51, Appl
417	49.2	2.1	302250	9	US-09-962-832-154	Sequence 154, App	490	48.2	2.0	3476	15	US-10-238-411-51	Sequence 51, Appl
418	49	2.1	5430	13	US-10-312-841-1	Sequence 1, Appl	491	48.2	2.0	3476	15	US-10-243-124-51	Sequence 51, Appl
419	49	2.1	6106	13	US-10-312-714A-14	Sequence 14, Appl	492	48.2	2.0	3476	15	US-10-243-425-51	Sequence 51, Appl
420	49	2.1	6106	15	US-10-311-455-1145	Sequence 151, App	493	48.2	2.0	3476	15	US-10-243-446-51	Sequence 51, Appl
421	49	2.1	15767	15	US-10-257-166-113	Sequence 1445, App	494	48.2	2.0	3476	15	US-10-245-874-51	Sequence 51, Appl
422	49	2.1	15767	15	US-10-311-455-1180	Sequence 113, App	495	48.2	2.0	3476	15	US-10-242-653-51	Sequence 51, Appl
423	48.8	2.1	9810	15	US-10-240-485-106	Sequence 1180, App	496	48.2	2.0	3476	15	US-10-243-167-51	Sequence 51, Appl
424	48.8	2.1	12025	15	US-10-311-455-399	Sequence 106, App	497	48.2	2.0	3476	15	US-10-243-388-51	Sequence 51, Appl
425	48.8	2.1	13202	15	US-10-311-455-1272	Sequence 399, App	498	48.2	2.0	3476	15	US-10-244-947-51	Sequence 51, Appl
426	48.8	2.1	13712	15	US-10-311-455-1458	Sequence 1272, App	499	48.2	2.0	3476	15	US-10-244-968-51	Sequence 51, Appl
427	48.6	2.0	6154	13	US-10-311-455-1503	Sequence 1458, App	500	48.2	2.0	3476	15	US-10-244-990-51	Sequence 51, Appl
428	48.6	2.0	11172	15	US-10-221-613-69	Sequence 1503, App	501	48.2	2.0	3476	15	US-10-245-079-51	Sequence 51, Appl
429	48.6	2.0	17137	15	US-10-311-455-2026	Sequence 59, Appl	502	48.2	2.0	3476	15	US-10-245-127-51	Sequence 51, Appl
430	48.6	2.0	367378	15	US-10-311-455-164	Sequence 2026, App	503	48.2	2.0	3476	15	US-10-245-207-51	Sequence 51, Appl
431	48.4	2.0	643	13	US-10-424-599-106363	Sequence 164, App	504	48.2	2.0	3476	15	US-10-245-646-51	Sequence 51, Appl
432	48.4	2.0	6775	17	US-10-433-793-190	Sequence 1, Appl	505	48.2	2.0	3476	15	US-10-245-695-51	Sequence 51, Appl
433	48.4	2.0	640681	9	US-09-790-988-1	Sequence 190, App	506	48.2	2.0	3476	15	US-10-245-699-51	Sequence 51, Appl
434	48.2	2.0	334	15	US-10-029-386-26472	Sequence 1, Appl	507	48.2	2.0	3476	15	US-10-245-737-51	Sequence 51, Appl
435	48.2	2.0	538	15	US-10-029-386-12772	Sequence 26472, A	508	48.2	2.0	3476	15	US-10-245-878-51	Sequence 51, Appl
436	48.2	2.0	538	15	US-10-029-386-12772	Sequence 12772, A	509	48.2	2.0	3476	15	US-10-245-890-51	Sequence 51, Appl
437	48.2	2.0	972	9	US-09-764-853-156	Sequence 156, App	510	48.2	2.0	3476	15	US-10-243-899-51	Sequence 51, Appl
438	48.2	2.0	1720	9	US-09-981-876-53	Sequence 53, App	511	48.2	2.0	3476	15	US-10-243-899-51	Sequence 51, Appl
439	48.2	2.0	1720	10	US-09-148-545-53	Sequence 53, App	512	48.2	2.0	3476	15	US-10-245-900-51	Sequence 51, Appl
440	48.2	2.0	2013	10	US-09-759-130B-330	Sequence 330, App	513	48.2	2.0	3476	15	US-10-247-058-51	Sequence 51, Appl
441	48.2	2.0	2013	15	US-10-189-123-60	Sequence 60, App	514	48.2	2.0	3476	15	US-10-245-454-51	Sequence 51, Appl
442	48.2	2.0	2013	15	US-10-188-495-60	Sequence 60, App	515	48.2	2.0	3476	15	US-10-237-471-51	Sequence 51, Appl
443	48.2	2.0	2013	17	US-10-741-790-330	Sequence 60, App	516	48.2	2.0	3476	15	US-10-238-261-51	Sequence 51, Appl
444	48.2	2.0	2558	10	US-09-983-000A-13	Sequence 330, App	517	48.2	2.0	3476	15	US-10-238-324-51	Sequence 51, Appl
445	48.2	2.0	2694	15	US-10-050-704-40	GENERAL INFORMATI	518	48.2	2.0	3476	15	US-10-241-860-51	Sequence 51, Appl
446	48.2	2.0	2694	17	US-10-798-512-40	Sequence 40, App	519	48.2	2.0	3476	15	US-10-242-172-51	Sequence 51, Appl
447	48.2	2.0	2730	15	US-09-759-130B-329	Sequence 40, App	520	48.2	2.0	3476	15	US-10-242-652-51	Sequence 51, Appl
448	48.2	2.0	2730	15	US-10-189-123-59	Sequence 329, App	521	48.2	2.0	3476	15	US-10-242-990-51	Sequence 51, Appl
449	48.2	2.0	2730	15	US-10-188-495-59	Sequence 59, App	522	48.2	2.0	3476	15	US-10-243-023-51	Sequence 51, Appl
450	48.2	2.0	2878	17	US-10-741-790-329	Sequence 329, App	523	48.2	2.0	3476	15	US-10-243-103-51	Sequence 51, Appl
451	48.2	2.0	2878	13	US-10-453-420-7	Sequence 7, Appl	524	48.2	2.0	3476	15	US-10-243-276-51	Sequence 51, Appl
452	48.2	2.0	3438	13	US-10-295-027-259	Sequence 259, App	525	48.2	2.0	3476	15	US-10-243-364-51	Sequence 51, Appl
					Sequence 60, App	Sequence 60, App							

526	48.2	2.0	3476	15	US-10-244-995-51	Sequence 51, Appl	599	46.8	2.0	3153	10	US-09-759-130B-343	Sequence 343, App
527	48.2	2.0	3476	15	US-10-245-230-51	Sequence 51, Appl	600	46.8	2.0	3153	15	US-10-189-123-73	Sequence 73, Appl
528	48.2	2.0	3476	15	US-10-245-253-51	Sequence 51, Appl	601	46.8	2.0	3153	15	US-10-189-495-73	Sequence 73, Appl
529	48.2	2.0	3476	15	US-10-245-479-51	Sequence 51, Appl	602	46.8	2.0	3153	17	US-10-741-790-343	Sequence 343, App
530	48.2	2.0	3476	15	US-10-245-499-51	Sequence 51, Appl	603	46.8	2.0	5987	15	US-10-311-455-1536	Sequence 1536, App
531	48.2	2.0	3476	15	US-10-245-772-51	Sequence 51, Appl	604	46.8	2.0	5987	17	US-10-433-793-132	Sequence 132, App
532	48.2	2.0	3476	15	US-10-245-811-51	Sequence 51, Appl	605	46.8	2.0	6301	15	US-10-311-455-25	Sequence 25, Appl
533	48.2	2.0	3476	15	US-10-245-812-51	Sequence 51, Appl	606	46.8	2.0	6301	15	US-10-221-613-114	Sequence 114, App
534	48.2	2.0	3476	15	US-10-245-852-51	Sequence 51, Appl	607	46.8	2.0	9760	13	US-10-221-613-114	Sequence 114, App
535	48.2	2.0	3476	15	US-10-245-852-51	Sequence 51, Appl	608	46.8	2.0	12968	13	US-10-221-714A-506	Sequence 506, App
536	48.2	2.0	3476	15	US-10-245-852-51	Sequence 51, Appl	609	46.8	2.0	12968	15	US-10-239-676-202	Sequence 202, App
537	48.2	2.0	3476	15	US-10-245-881-51	Sequence 51, Appl	610	46.8	2.0	12968	15	US-10-311-455-2058	Sequence 2058, App
538	48.2	2.0	3476	15	US-10-245-911-51	Sequence 51, Appl	611	46.8	2.0	12968	15	US-10-240-453-298	Sequence 298, App
539	48.2	2.0	3476	15	US-10-245-913-51	Sequence 51, Appl	612	46.8	2.0	960	15	US-10-198-846-6381	Sequence 6381, App
540	48.2	2.0	3476	15	US-10-246-080-51	Sequence 51, Appl	613	46.8	2.0	2747	9	US-09-917-800A-1588	Sequence 1588, App
541	48.2	2.0	3476	15	US-10-246-121-51	Sequence 51, Appl	614	46.8	2.0	5163	15	US-10-311-455-1221	Sequence 1221, App
542	48.2	2.0	3476	15	US-10-246-305-51	Sequence 51, Appl	615	46.8	2.0	7676	15	US-10-240-485-151	Sequence 151, App
543	48.2	2.0	3476	15	US-10-246-929-51	Sequence 51, Appl	616	46.8	2.0	9180	15	US-10-311-455-1937	Sequence 1937, App
544	48.2	2.0	3476	15	US-10-247-036-51	Sequence 51, Appl	617	46.8	2.0	10891	15	US-10-311-455-438	Sequence 438, App
545	48.2	2.0	3476	15	US-10-243-255-51	Sequence 51, Appl	618	46.8	2.0	11092	15	US-10-311-455-1485	Sequence 1485, App
546	48.2	2.0	3476	15	US-10-245-810-51	Sequence 51, Appl	619	46.8	2.0	12507	15	US-10-311-455-271	Sequence 271, App
547	48.2	2.0	3476	15	US-10-246-098-51	Sequence 51, Appl	620	46.8	2.0	15548	15	US-10-311-455-2128	Sequence 2128, App
548	48.2	2.0	3476	15	US-10-237-496-51	Sequence 51, Appl	621	46.8	2.0	40862	15	US-10-311-455-2046	Sequence 2046, App
549	48.2	2.0	3476	15	US-10-242-074-51	Sequence 51, Appl	622	46.8	2.0	4172	15	US-10-311-455-687	Sequence 687, App
550	48.2	2.0	3476	15	US-10-242-505-51	Sequence 51, Appl	623	46.8	2.0	6040	15	US-10-204-708-70	Sequence 70, Appl
551	48.2	2.0	3476	15	US-10-242-574-51	Sequence 51, Appl	624	46.8	2.0	6040	17	US-10-240-589C-110	Sequence 110, App
552	48.2	2.0	3476	15	US-10-243-261-51	Sequence 51, Appl	625	46.8	2.0	16228	13	US-10-221-613-387	Sequence 387, App
553	48.2	2.0	3476	15	US-10-243-282-51	Sequence 51, Appl	626	46.8	2.0	17594	15	US-10-311-455-1999	Sequence 1999, App
554	48.2	2.0	3476	15	US-10-243-403-51	Sequence 51, Appl	627	46.8	2.0	19131	13	US-10-221-714A-442	Sequence 442, App
555	48.2	2.0	3476	15	US-10-243-431-51	Sequence 51, Appl	628	46.8	2.0	471	13	US-10-424-599-112213	Sequence 112213
556	48.2	2.0	3476	15	US-10-245-164-51	Sequence 51, Appl	629	46.8	2.0	5880	15	US-10-240-453-51	Sequence 53, Appl
557	48.2	2.0	3476	15	US-10-244-972-51	Sequence 51, Appl	630	46.8	2.0	5981	15	US-10-311-455-1736	Sequence 1736, App
558	48.2	2.0	3476	15	US-10-197-942-51	Sequence 51, Appl	631	46.8	2.0	6831	15	US-10-311-455-1460	Sequence 1460, App
559	48.2	2.0	3476	15	US-10-238-196-51	Sequence 51, Appl	632	46.8	2.0	12507	15	US-10-311-455-1460	Sequence 1460, App
560	48.2	2.0	3476	15	US-10-245-013-51	Sequence 51, Appl	633	46.8	2.0	15743	15	US-10-240-453-270	Sequence 270, App
561	48.2	2.0	5430	15	US-10-091-438-279	Sequence 279, App	634	46.8	2.0	19380	13	US-10-221-613-390	Sequence 390, App
562	48.2	2.0	6106	13	US-10-221-714A-151	Sequence 151, App	635	46.8	2.0	3057	15	US-10-349-680-148	Sequence 148, App
563	48.2	2.0	6106	15	US-10-311-455-1445	Sequence 1445, App	636	46.8	2.0	4611	17	US-10-433-793-51	Sequence 51, Appl
564	48.2	2.0	6106	17	US-10-257-166-113	Sequence 113, Appl	637	46.8	2.0	6113	15	US-10-204-708-13	Sequence 13, Appl
565	48.2	2.0	9646	13	US-10-462-261-1	Sequence 1, Appl	638	46.8	2.0	6113	15	US-10-311-455-403	Sequence 403, App
566	48.2	2.0	5362	15	US-10-240-453-288	Sequence 288, App	639	46.8	2.0	6113	17	US-10-240-589C-13	Sequence 13, Appl
567	47.8	2.0	650	13	US-10-027-632-231715	Sequence 231715, App	640	46.8	2.0	9095	17	US-10-433-793-92	Sequence 92, Appl
568	47.8	2.0	650	13	US-10-027-632-231716	Sequence 231716, App	641	46.8	2.0	9524	15	US-10-311-455-812	Sequence 812, App
569	47.8	2.0	650	13	US-10-027-632-231717	Sequence 231717, App	642	46.8	2.0	9524	17	US-10-257-166-76	Sequence 76, Appl
570	47.8	2.0	650	16	US-10-027-632-231715	Sequence 231715, App	643	46.8	2.0	14316	13	US-10-221-613-408	Sequence 408, App
571	47.8	2.0	650	16	US-10-027-632-231716	Sequence 231716, App	644	46.8	2.0	15587	13	US-10-221-613-198	Sequence 198, App
572	47.8	2.0	650	16	US-10-027-632-231717	Sequence 231717, App	645	46.8	2.0	16217	15	US-10-311-455-598	Sequence 598, App
573	47.6	2.0	9965	15	US-10-311-455-1500	Sequence 1500, App	646	46.8	2.0	21537	15	US-10-311-455-1971	Sequence 1971, App
574	47.6	2.0	12578	13	US-10-221-714A-382	Sequence 382, App	647	45.8	1.9	5520	15	US-10-172-086-31	Sequence 31, Appl
575	47.6	2.0	12781	13	US-10-221-714A-107	Sequence 107, App	648	45.8	1.9	5659	15	US-10-311-455-347	Sequence 347, App
576	47.6	2.0	12781	17	US-10-240-589C-37	Sequence 37, Appl	649	45.8	1.9	5659	15	US-10-311-455-39	Sequence 39, Appl
577	47.4	2.0	40862	15	US-10-311-455-2046	Sequence 2046, App	650	45.8	1.9	5659	15	US-10-240-485-33	Sequence 33, Appl
578	47.4	2.0	161671	15	US-10-017-117-1	Sequence 1, Appl	651	45.8	1.9	6065	17	US-10-311-455-478	Sequence 478, App
579	47.2	2.0	960	15	US-10-198-846-6381	Sequence 6381, App	652	45.8	1.9	6072	15	US-10-311-455-3	Sequence 3, Appl
580	47.2	2.0	5413	13	US-10-221-714A-418	Sequence 418, App	653	45.8	1.9	6120	15	US-10-311-455-466	Sequence 466, App
581	47.2	2.0	6074	15	US-10-240-453-248	Sequence 248, App	654	45.8	1.9	6361	15	US-10-311-455-1113	Sequence 1113, App
582	47.2	2.0	6174	13	US-10-221-714A-155	Sequence 155, App	655	45.8	1.9	7498	15	US-10-311-455-230	Sequence 230, App
583	47.2	2.0	6191	15	US-10-311-455-1189	Sequence 1189, App	656	45.8	1.9	7498	15	US-10-311-455-1564	Sequence 1564, App
584	47.2	2.0	7669	15	US-10-311-455-601	Sequence 601, App	657	45.8	1.9	10279	17	US-10-240-589C-86	Sequence 86, Appl
585	47.2	2.0	17137	15	US-10-311-455-164	Sequence 164, App	658	45.8	1.9	10279	17	US-10-240-589C-86	Sequence 86, Appl
586	47.2	2.0	17137	15	US-10-221-714A-387	Sequence 387, App	659	45.8	1.9	11260	15	US-10-239-676-20	Sequence 20, Appl
587	47.2	2.0	513509	13	US-09-754-853A-4	Sequence 4, Appl	660	45.8	1.9	11260	15	US-10-240-453-28	Sequence 28, Appl
588	47.2	2.0	4045	13	US-10-221-714A-466	Sequence 466, App	661	45.8	1.9	11996	15	US-10-240-485-46	Sequence 46, Appl
589	47.2	2.0	5006	9	US-09-837-751-7	Sequence 7, Appl	662	45.4	1.9	628	13	US-10-027-632-113152	Sequence 113152
590	47.2	2.0	7057	13	US-10-221-613-317	Sequence 317, App	663	45.4	1.9	628	16	US-09-129-112-3	Sequence 3, Appl
591	47.2	2.0	7057	13	US-10-221-714A-323	Sequence 323, App	664	45.4	1.9	7498	15	US-10-311-455-230	Sequence 230, App
592	47.2	2.0	7057	13	US-10-311-455-1821	Sequence 1821, App	665	45.4	1.9	9881	15	US-10-240-452-54	Sequence 54, Appl
593	47.2	2.0	7057	17	US-10-240-485-147	Sequence 147, App	666	45.4	1.9	9881	15	US-10-311-455-1564	Sequence 1564, App
594	47.2	2.0	11964	17	US-10-433-793-55	Sequence 55, Appl	667	45.4	1.9	10279	17	US-10-240-589C-86	Sequence 86, Appl
595	47.2	2.0	16258	17	US-10-257-166-120	Sequence 120, App	668	45.4	1.9	10279	17	US-10-240-589C-86	Sequence 86, Appl
596	47.2	2.0	172569	13	US-10-087-1362-1366	Sequence 1366, App	669	45.4	1.9	11260	15	US-10-239-676-20	Sequence 20, Appl
597	46.8	2.0	319	10	US-09-814-353-6115	Sequence 6115, App	670	45.4	1.9	11260	15	US-10-240-453-28	Sequence 28, Appl
598	46.8	2.0	319	10	US-09-814-353-6115	Sequence 6115, App	671	45.4	1.9	11996	15	US-10-240-485-46	Sequence 46, Appl
599	46.8	2.0	319	10	US-09-814-353-6115	Sequence 6115, App	672	45.4	1.9	11996	15	US-10-240-485-46	Sequence 46, Appl

672	45.4	1.9	13420	15	US-10-311-455-890	Sequence 890, App	745	44.2	1.9	9515	15	US-10-240-453-182	Sequence 182, App
673	45.4	1.9	40324	17	US-10-433-793-179	Sequence 179, App	746	44.2	1.9	11187	15	US-10-240-453-326	Sequence 326, App
674	45.2	1.9	11029	13	US-10-424-599-134182	Sequence 134182, App	747	44.2	1.9	18283	13	US-10-221-613-325	Sequence 325, App
675	45.2	1.9	2432	15	US-10-198-846-12893	Sequence 12893, A	748	44.2	1.9	33053	17	US-10-433-793-36	Sequence 36, App
676	45.2	1.9	5267	17	US-10-433-793-73	Sequence 73, Appl	749	44.2	1.9	198522	13	US-10-087-192-244	Sequence 244, App
677	45.2	1.9	8876	15	US-10-311-455-2049	Sequence 2049, Ap	750	44	1.9	419	9	US-09-960-353-11234	Sequence 11234, A
678	45.2	1.9	17183	15	US-10-311-455-460	Sequence 460, App	751	44	1.9	3007	15	US-10-239-676-219	Sequence 219, App
679	45.2	1.9	17419	15	US-10-239-676-100	Sequence 100, App	752	44	1.9	3007	15	US-10-240-453-319	Sequence 319, App
680	45.2	1.9	17419	15	US-10-311-455-1268	Sequence 1268, Ap	753	44	1.9	3151	17	US-10-433-793-174	Sequence 174, App
681	45.2	1.9	17419	15	US-10-240-453-112	Sequence 112, App	754	44	1.9	5820	15	US-10-311-455-511	Sequence 511, App
682	45	1.9	535	17	US-10-021-323-1934	Sequence 1934, Ap	755	44	1.9	6129	13	US-10-221-613-108	Sequence 108, App
683	45	1.9	12142	15	US-10-311-455-1646	Sequence 1646, Ap	756	44	1.9	6306	15	US-10-239-676-129	Sequence 129, App
684	45	1.9	14987	15	US-10-311-455-603	Sequence 603, App	757	44	1.9	7327	15	US-10-311-455-1233	Sequence 1233, Ap
685	45	1.9	18133	15	US-10-311-455-914	Sequence 914, App	758	44	1.9	7327	15	US-10-221-613-299	Sequence 299, App
686	45	1.9	18133	17	US-10-257-166-100	Sequence 100, App	759	44	1.9	7522	15	US-10-311-455-887	Sequence 887, App
687	45	1.9	19659	15	US-10-311-455-739	Sequence 739, App	760	44	1.9	7597	15	US-10-311-455-986	Sequence 986, App
688	44.8	1.9	4661	17	US-10-433-793-52	Sequence 52, Appl	761	44	1.9	8952	13	US-10-221-714A-167	Sequence 167, App
689	44.8	1.9	5593	15	US-10-311-455-1134	Sequence 1134, Ap	762	44	1.9	11964	17	US-10-433-793-56	Sequence 56, Appl
690	44.8	1.9	6759	15	US-10-311-455-711	Sequence 711, App	763	44	1.9	13627	17	US-10-433-793-5	Sequence 5, Appl
691	44.8	1.9	7231	15	US-10-240-453-23	Sequence 23, Appl	764	44	1.9	17674	15	US-10-311-455-318	Sequence 318, Ap
692	44.8	1.9	10048	17	US-10-433-793-45	Sequence 45, Appl	765	44	1.9	56153	13	US-10-433-287-520	Sequence 520, App
693	44.8	1.9	20579	17	US-10-433-793-104	Sequence 104, App	766	44	1.9	95109	17	US-10-221-714A-50	Sequence 80, Appl
694	44.6	1.9	641	13	US-10-027-632-113326	Sequence 113326, A	767	44	1.9	449	16	US-10-085-783A-30386	Sequence 30386, A
695	44.6	1.9	641	16	US-10-027-632-113326	Sequence 113326, A	768	43.8	1.8	449	13	US-10-242-535A-30386	Sequence 30386, A
696	44.6	1.9	5979	15	US-10-239-676-18	Sequence 18, Appl	769	43.8	1.8	5487	15	US-10-311-455-1571	Sequence 1571, Ap
697	44.6	1.9	5979	15	US-10-240-453-26	Sequence 26, Appl	770	43.8	1.8	6127	15	US-10-240-485-1	Sequence 1, Appl
698	44.6	1.9	6063	15	US-10-240-453-268	Sequence 268, App	771	43.8	1.8	6233	13	US-10-221-714A-219	Sequence 219, App
699	44.6	1.9	6759	15	US-10-311-455-712	Sequence 712, App	772	43.8	1.8	6418	13	US-10-221-613-30	Sequence 30, Appl
700	44.6	1.9	13784	17	US-10-257-166-143	Sequence 143, App	773	43.8	1.8	6418	15	US-10-311-455-296	Sequence 296, App
701	44.6	1.9	14649	15	US-10-239-676-121	Sequence 121, App	774	43.8	1.8	8227	15	US-10-240-485-94	Sequence 94, Appl
702	44.6	1.9	14649	15	US-10-240-453-141	Sequence 141, App	775	43.8	1.8	8227	17	US-10-433-793-156	Sequence 156, App
703	44.6	1.9	16236	15	US-10-311-455-995	Sequence 995, App	776	43.8	1.8	11996	15	US-10-240-485-45	Sequence 45, Appl
704	44.6	1.9	18283	13	US-10-221-613-326	Sequence 326, Appl	777	43.8	1.8	12237	15	US-10-311-455-2331	Sequence 2331, Ap
705	44.6	1.9	96589	12	US-09-997-722-46	Sequence 46, Appl	778	43.8	1.8	14861	13	US-10-221-613-161	Sequence 161, App
706	44.6	1.9	159400	17	US-10-450-826-33	Sequence 33, Appl	779	43.8	1.8	14861	13	US-10-221-613-161	Sequence 1167, Ap
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Job time : 1055 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM protein - nucleic search, using frame_plus_p2n model
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Searched: 3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	1657	100.0	2372	6	AR410761	Sequence
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9	1657	100.0	2372	6	AX454446	Sequence
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21	1174	70.9	1613	4	AY372937	Bos taurus
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ALIGNMENTS

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DEFINITION Homo sapiens hyaluronidic acid receptor (HAR) mRNA, complete cds.
ACCESSION AF127670
VERSION AF127670.2 GI:10800121
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1285)
AUTHORS Winkelmann, J.C., Basu, S., Ozdemir, E. and Blough, R.I.
TITLE HAR: a novel homolog of CD44 and putative hyaluronidic acid receptor encoded by a gene on human chromosome 11p15
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1009)
AUTHORS Winkelmann, J.C., Basu, S., Ozdemir, E. and Blough, R.I.
TITLE Direct Submission
JOURNAL Submitted (11-FEB-1999) Hematology-Oncology, University of Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, USA
REFERENCE 3 (bases 1 to 1285)
AUTHORS Winkelmann, J.C., Basu, S., Ozdemir, E. and Blough, R.I.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-1999) Hematology-Oncology, University of Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, USA
REMARK Sequence update by submitter
COMMENT On Oct 13, 2000 this sequence version replaced gi:5732667.
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gene
CDS

ORIGIN

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Score: 1657.00 Matches: 322
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US-10-063-670-6 (1-322) x AF127670 (1-1285)

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AX136227 1755 bp DNA linear PAT 30-MAY-2001
LOCUS AX136227
DEFINITION Sequence 149 from Patent EP1067182.
ACCESSION AX136227
VERSION AX136227.1 GI:14272635
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 149 10-JAN-2001;
Helix Research Institute (JP)

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CDS

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CDS

Alignment Scores:
Pred. No.: 2,42e-127 Length: 1755
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Query Match: 100.00% Indels: 0
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QY 61 CysArgLeuLeuGlyLeuSerIleuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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RESULT 4

AK075443

LOCUS

DEFINITION Homo sapiens cDNA PSEC0135 fis, clone PLACE1004850, highly similar to Homo sapiens lymphatic endothelium-specific hyaluronan receptor LYVE-1 mRNA.

ACCESSION

AK075443

VERSION

AK075443.1 GI:22761535

KEYWORDS

oligo capping, fis (full insert sequence).

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

HRI human cDNA sequencing project

AUTHORS

Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K., Ishii, S., Saito, K., Yamamoto, J., Wakamatsu, A., Nagai, T., Nakamura, Y., Nagahari, K., Sugano, S. and Isogai, T.

TITLE

HRI human cDNA sequencing project

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 1755)

AUTHORS

Isogai, T. and Yamamoto, J.

TITLE

Direct Submission

JOURNAL

Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

COMMENT

HRI human cDNA sequencing project: cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing: Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center. Location/Qualifiers

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Best Local Similarity:	100.00%	Mismatches:	0
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US-10-063-670-6 (1-322) x AK075443 (1-1755)

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SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 REFERENCE 1 (bases 1 to 2029)
 AUTHORS Lal, P., Tang, Y.T., Gorgone, G.A., Corley, N.C., Guegler, K.J., Baughn, M.R., Akerblom, I.E., Young, J.A., Yue, H., Patterson, C., Reddy, R., Hillman, J.B. and Bandman, O.
 TITLE Human signal peptide-containing protein
 JOURNAL Patent: JP 2002519030-A 64 02-JUL-2002;
 INCVTE PHARMACEUTICALS INC
 COMMENT OS Homo sapiens (human)
 PN JP 2002519030-A/64
 PD 02-JUL-2002
 PF 25-JUN-1999 JP 2000557363
 PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR 01-OCT-1998 US 60/102686,11-DEC-1998 US 60/112129 PI PRETTI LAL, Y TOM TANG, GINA A GORGONE, NEIL C CORLEY, KARL J PI GUEGLER, PI MARIAH R BAUGHN, INGRID E AKERBLOM, JANICE AU YOUNG, HENRY YUE, PI CHANDRA PATTERSON, ROOPA REDDY, JENNIFER L HILLMAN, OLGA BANDMAN PC C12N15/09, A61K38/00, A61K39/395, A61K45/00, A61P9/00, A61P15/00, A61P25/00, A61P29/00, A61P35/00, A61P43/00, C07K14/47, C07K16/18, C12N1/15, PC C12N1/19, PC C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N33/68//C12P21/08, PC C12N15/00, PC A61K37/02, C12N5/00
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 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 2372)
 Ashkenazi, A., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, D.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
 JOURNAL Patent: US 6635468-A 200 21-OCT-2003;
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AX092274 ACCESSION
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SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
AUTHORS Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 5 08-MAR-2001;
Genentech, Inc. (US)
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Pred. No.: 3,566-127 Matches: 322
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US-10-063-670-6 (1-322) x AX092274 (1-2372)
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QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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VERSION     AX490924.1  GI:22323799
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ORGANISM    Homo sapiens
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  AUTHORS   Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
            Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
            Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
            and Ye, W.
  TITLE     Compositions and methods for the diagnosis and treatment of
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  JOURNAL   Patent: WO 020690-A 31 03-JAN-2002;
            Genentech, Inc. (US)
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US-10-063-670-6 (1-322) x AX490924 (1-2372)

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  AUTHORS   Ashkenazi, A.J., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N.,
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  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
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1 (bases 1 to 2372)
 Wood, W.I., Gurney, A.L., Goddard, A., Penica, D., Chen, J. and Yuan, J.
 Secretory and transmembrane polypeptide and nucleic acid encoding
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 Patent: JP 2001516580-A 165 02-OCT-2001;
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 25-NOV-1997 US 60/066840
 PI WILLIAM I WOOD, AUSTIN L GURNEY, AUDLEY GODDARD, DIANE PENICA, PI
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 PI C12N15/09, C07K14/47, C07K16/705, C07K16/18, C07K19/00,
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ACCESSION BD172392
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2372)

AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
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GENENTECH INC
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PN JP 2002223786-A/165
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PI JEAN YUAN
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 BD172711.1 GI:28414015
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 SOURCE
 Homo sapiens
 ORGANISM
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 2372)

AUTHORS

Wood, W. I., Gurney, A. L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.

Secretd and transmembrane polypeptides and nucleic acids encoding the same

PATENT: JP 2002238586-A 165 27-AUG-2002;

JOURNAL

GENETECH INC

COMMENT

OS Homo sapiens (human)

PN JP 2002238586-A/165

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385205

PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR

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07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR

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24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066940 PI

WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC

C12N5/10,

PC C12P21/02/C12P21/08,C12N1/19,C12R1/645),(C12N1/21,C12R1/19);

(C12N5/10,C12R1/91),(C12P21/02,C12R1/91),(C12P21/02,C12R1/645), PC

(C12P21/02,C12R1/19),(C12P21/08,C12R1/91),(C12N15/00,C12N5/00, PC

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encoding the same

FH Key Location/Qualifiers

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FEATURES

source 1..2372

/organism='Homo sapiens'

(C12P21/02,C12R1/19),(C12P21/08,C12R1/91),(C12P21/02,C12R1/645), PC

(C12N5/00,C12R1/91)

CC Secretd and transmembrane polypeptides and nucleic CC

encoding the same

FH Key Location/Qualifiers

FT source 1..2372 /organism='Homo sapiens (human)'

ORIGIN

Alignment Scores:

Pred. No.: 3.56e-127 Length: 2372

Score: 1657.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-063-670-6 (1-322) x BD172711 (1-2372)

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Db 160 ATGGCCAGGTGCTTCAGCTGGTGGTGTCTTCTCATTCCATCTGGACACGAGGCTCTGTG 219

QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40

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Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
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DEFINITION	Secreted and transmembrane polypeptides and nucleic acids encoding the same.		
ACCESSION	BD173030		
VERSION	BD173030.1	GI:28414336	
KEYWORDS	JP 2002238587-A/165.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 2372) Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: JP 2002238587-A 165 27-AUG-2002;		
COMMENT	GENENTECH INC OS Homo sapiens (human) PN JP 2002238587-A/165 PD 27-AUG-2002 PF 18-DEC-2001 JP 2001385248 PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR 17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR 21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR 24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR 27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR 28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR 28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR 29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR 31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR 07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR 17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR 21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR 24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR 24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR 24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PR WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI JIAN ZHENG, PI JEAN YUAN PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC C12N15/02, PC C12P21/02, C12P21/08// (C12P21/02, C12R1.91), (C12P21/02, C12R1.19), PC (C12P21/02, C12R1.645), C12N15/00, C12N5/00, C12N15/00 CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the same FH Key Location/Qualifiers FT source 1. .2372 /organism='Homo sapiens (human)'. FEATURES source 1. .2372 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" ORIGIN Alignment Scores: Pred. No.: 3,56e-127 Length: 2372 Score: 1657.00 Matches: 322 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 6 Gaps: 0 US-10-063-670-6 (1-322) x BD173030 (1-2372) Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20 Db 160 ATGCCAGGAGCTTCAGCCTGGTGTCTCTCATTCCATCTGGACACGAGGCTCCTG 219 Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40		

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Job time : 4669 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2004, 01:23:18 ; Search time 467 Seconds

(without alignments)

2929.164 Million cell updates/sec

Title: US-10-063-670-6

Perfect score: 1657

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Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 800 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1657	100.0	2029	3 AAZ98172	Aaz98172 Human sig
4	1657	100.0	2029	10 ADE71445	Ade71445 Human cDN
5	1657	100.0	2372	2 AAAX52250	Aax52250 Protein P
6	1657	100.0	2372	3 ADC78520	Adc78520 Human PRO
7	1657	100.0	2372	4 AAF72408	Aaf72408 Human PRO
8	1657	100.0	2372	4 AAF92060	Aaf92060 Human PRO

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62	1657	100.0	2372	9 ADB68064	AdB68064 Human PRO
63	1657	100.0	2372	9 ADB90881	AdB90881 Novel hum
64	1657	100.0	2372	9 ADC28508	AdC28508 Human sec
65	1657	100.0	2372	9 ADC39708	AdC39708 Human sec
66	1657	100.0	2372	9 ADC40222	AdC40222 Human sec
67	1657	100.0	2372	9 ADC19046	AdC19046 Human sec
68	1657	100.0	2372	9 ADC34346	AdC34346 Human sec
69	1657	100.0	2372	9 ADC29401	AdC29401 Human sec
70	1657	100.0	2372	9 ADC28932	AdC28932 Human sec
71	1657	100.0	2372	9 ADC40817	AdC40817 Human sec
72	1657	100.0	2372	9 ADC19474	AdC19474 Human sec
73	1657	100.0	2372	9 ADC06961	AdC06961 Human PRO
74	1657	100.0	2372	9 ADC17140	AdC17140 cDNA sequ
75	1657	100.0	2372	9 ADC33922	AdC33922 Human sec
76	1657	100.0	2372	9 ADC12992	AdC12992 Human sec
77	1657	100.0	2372	9 ADC14838	AdC14838 Novel hum
78	1657	100.0	2372	9 ADC52333	AdC52333 Novel hum
79	1657	100.0	2372	9 ADC12444	AdC12444 Human sec
80	1657	100.0	2372	9 ADD10320	AdD10320 Human sec
81	1657	100.0	2372	9 ADD11280	AdD11280 Human sec

82	1657	100.0	2372	9	ADD04005	Ad04005 Human sec	155	199.5	12.0	2308	3	AAA50598	Aaa50598 Human epi
83	1657	100.0	2372	9	ADD03581	Ad03581 Human sec	156	199.5	12.0	4674	7	ABX77520	Abx77520 Different
84	1657	100.0	2372	9	ADD37073	Ad37073 Human sec	157	197	11.9	2097	7	ADD90595	Add90595 Human CD4
85	1657	100.0	2372	9	ADD36009	Ad36009 Novel hum	158	197	11.9	2387	7	ABX76192	Abx76192 Lung canc
86	1657	100.0	2372	9	ADE34833	Ad34833 Human sec	159	197	11.9	2905	7	ABX63495	Abx63495 Human cDN
87	1657	100.0	2372	10	ADC52143	Adc52143 Novel hum	160	197	11.9	3474	8	ADAL0891	Ada10891 Human cDN
88	1657	100.0	2372	10	ADE79278	Ad79278 Human sec	161	191.5	11.6	3336	7	ACC43051	Acc43051 Nucleotid
89	1657	100.0	2372	10	ADE79702	Ad79702 Human sec	162	190	11.5	339	7	ACC43049	Acc43049 Nucleotid
90	1657	100.0	2372	10	ADE73378	Ad73378 Human sec	163	188	11.3	336	7	ACC43052	Acc43052 Nucleotid
91	1657	100.0	2372	10	ADE41281	Ad41281 Human sec	164	186	11.2	336	7	ACC43053	Acc43053 Nucleotid
92	1657	100.0	2372	10	ADE73913	Ad73913 Human sec	165	184	11.1	336	7	ACC43054	Acc43054 Nucleotid
93	1654	99.8	2324	4	ABA09223	Aba09223 Human PRO	166	182	11.0	336	7	ACC43050	Acc43050 Nucleotid
94	1651	99.6	2313	2	RAV22687	Rav22687 DNA encod	167	180.5	10.9	2764	5	RAS81254	Ras81254 DNA encod
95	1651	99.6	2369	6	ABL90698	Ab190698 Human pol	168	179	10.8	2273	5	AA81258	Aa81258 DNA encod
96	1547	93.4	2967	3	RAAC59803	Abc59803 Human sec	169	170	10.3	106	4	AAI46523	Aai46523 Probe #15
97	1531	92.4	1680	9	ADD04999	Ad04999 Human sec	170	170	10.3	106	6	ABS14478	Abs14478 Human gen
98	1511.5	91.2	1127	7	ACA10111	Ac10111 Human NOV	171	166.5	10.0	399	8	ACH49200	Ach49200 Human leu
99	1103	66.6	1896	4	AAD10132	Ad10132 Mouse lym	172	165	10.0	820	10	ADE71448	Ade71448 Dog cDNA
100	1103	66.6	1896	6	ABL35066	Ab135066 Murine cD	173	158	9.5	549	6	ABZ34973	Abz34973 Human gen
101	901	54.4	596	6	ABT09892	Abt09892 Human bre	174	158	9.5	549	7	ABZ91738	Abz91738 Human nuc
102	803	48.5	716	5	AAF94017	Aaf94017 Primer sp	175	151	9.1	2863	9	ADB62456	Adb62456 Human cDN
103	673	40.6	411	8	ACH20895	Ach20895 Human adu	176	148.5	9.0	425	8	ACH48521	Ach48521 Human leu
104	595.5	35.9	559	10	ADE71446	Ade71446 Rat cDNA	177	145.5	8.8	781	7	ABX74436	Abx74436 Human cDN
105	592	35.7	451	2	AAX41156	Aax41156 Human sec	178	145.5	8.8	1144	7	ABX63446	Abx63446 Human cDN
106	440	26.6	486	8	ACH22904	Act22904 Human adu	179	145.5	8.8	1144	9	ADE25720	Ade25720 Human cDN
107	386	23.3	279	10	ADE71447	Ade71447 Rat cDNA	180	145.5	8.8	1422	7	ACC72678	Acc72678 Human can
108	306	18.5	469	4	ABA54110	Aba54110 Human foe	181	145.5	8.8	1422	7	ABX76382	Abx76382 Lung canc
109	306	18.5	469	4	AAI33763	Aai33763 Probe #24	182	145	8.8	1728	7	ABX63445	Abx63445 Human cDN
110	306	18.5	469	4	ABA23859	Ab23859 Probe #23	183	145	8.8	351	6	ABV95472	Abv95472 Human pan
111	306	18.5	469	4	AAK27829	Aak27829 Human bon	184	145	8.8	1414	2	AAQ27190	Aaq27190 Tumour ne
112	306	18.5	469	4	ABS27409	Ab27409 Human liv	185	145	8.8	1414	2	AAV71778	Aav71778 Tumour ne
113	306	18.5	469	6	ABS02280	Ab202280 Human gen	186	145	8.8	1414	4	AAD06019	Aad06019 Human tum
114	285	17.2	363	2	AAX41003	Aax41003 Human sec	187	145	8.8	1414	6	ABS54635	Ab54635 Human cDN
115	281.5	17.0	457	4	AAI33382	Aai33382 Probe #20	188	144	8.7	3366	7	AD48132	Ad48132 Rat CD44i
116	281.5	17.0	457	6	ABS01959	Ab201959 Human gen	189	143.5	8.7	396	8	ACH30555	Ach30555 Human tes
117	277	16.7	373	2	AAX51631	Aax51631 Human sec	190	142.5	8.6	8444	6	ABT08487	Abt08487 Human nov
118	234.5	14.2	1537	2	AAQ06236	Aaq06236 B7 adhesi	191	141.5	8.5	3625	4	AAF87120	Aaf87120 NOV9 codi
119	233.5	14.1	1089	6	ABN86523	Abn86523 Nucleotid	192	141.5	8.5	8495	6	ABT08488	Abt08488 Human nov
120	231	13.9	2747	6	ABN86507	Abn86507 Rat glyco	193	138.5	8.4	1411	4	AAH23114	Aah23114 Osteocarth
121	231	13.9	2747	6	ABK63681	Abk63681 Rat seque	194	137	8.3	3260	6	ABT08489	Abt08489 Human nov
122	229.5	13.9	1177	6	ABN86522	Abn86522 Nucleotid	195	137	8.3	4576	6	ABA04662	Aba04662 Human Hya
123	224	13.5	3207	2	AAQ14263	Aaq14263 p-met-1	196	137	8.3	4642	7	ABX13822	Abx13822 cDNA enco
124	223	13.4	191	6	ABZ35325	Abz35325 Human gen	197	137	8.3	4962	7	ABX13823	Abx13823 cDNA enco
125	222	13.4	141	4	ABA66678	Aba66678 Human foe	198	136	8.2	4706	6	ABA04648	Aba04648 Rat Hyalu
126	222	13.4	141	4	AAI45691	Aai45691 Probe #15	199	136	8.2	4706	7	ABX13821	Abx13821 cDNA enco
127	222	13.4	141	4	ABA33740	Aba33740 Probe #12	200	135.5	8.2	3153	4	Aaf29464	Aaf29464 Murine br
128	222	13.4	141	4	AAK40837	Aak40837 Human bon	201	135.5	8.2	3153	7	ACD66770	Acd66770 Secreted
129	222	13.4	141	4	ABS40414	Ab240414 Human liv	202	135.5	8.2	3153	8	ADB90788	Adb90788 Mouse cDN
130	222	13.4	141	6	ABS14788	Ab214788 Human gen	203	133.5	8.1	1734	6	ABS70406	Ab270406 Human bon
131	215	13.0	1354	2	AAQ21185	Aaq21185 Clone CD4	204	132.5	8.0	2160	9	ADB63670	Adb63670 Human cDN
132	215	13.0	1354	2	AAT14724	Aat14724 Human hae	205	131.5	7.9	2652	7	ABZ81727	Abz81727 Rat mutan
133	215	13.0	1354	2	AAV63461	Aav63461 Human CD4	206	131	7.9	2013	4	AAF29460	Aaf29460 Human TAN
134	215	13.0	1354	2	AAV81218	Aav81218 Human CD4	207	131	7.9	2013	7	ACD66767	Acd66767 Secreted
135	215	13.0	1354	3	AAA50597	Aaa50597 Human hae	208	131	7.9	2013	8	ADB90775	Adb90775 Human TAN
136	213	13.0	1354	4	AAAS0191	Aas0191 Human hae	209	131	7.9	2730	4	AAF29459	Aaf29459 Human TAN
137	213	12.9	1794	3	AAA52811	Aaa52811 Human CD4	210	131	7.9	2730	7	ACD66766	Acd66766 Secreted
138	213	12.9	1794	6	ABV94385	Abv94385 Breast ca	211	131	7.9	2730	8	ADB90774	Adb90774 Human cDN
139	213	12.9	1794	6	ABK84043	Abk84043 Human cDN	212	131	7.9	3476	4	AA91017	Aaa91017 Human sec
140	212	12.8	1083	9	ADD90591	Add90591 Human CD4	213	131	7.9	3476	6	ABK69986	Abk69986 cDNA enco
141	212	12.8	1807	7	AAD48131	Aad48131 Human CD4	214	131	7.9	3476	8	ADA01319	Ada01319 Human PRO
142	212	12.8	4365	9	ADE25668	Ade25668 Human cDN	215	131	7.9	3476	8	ADA43748	Ada43748 Human cDN
143	210	12.7	1297	6	ABN86521	Abn86521 Nucleotid	216	131	7.9	3476	8	ADA43516	Ada43516 Human cDN
144	203	12.3	1483	5	AAA91130	Aaa91130 CD44Hextr	217	131	7.9	3476	8	ADA01191	Ada01191 Human PRO
145	202.5	12.2	1468	5	AAA91129	Aaa91129 CD44Hextr	218	131	7.9	3476	8	ADA01075	Ada01075 Human cDN
146	199.5	12.0	1737	6	ABN86520	Abn86520 Nucleotid	219	131	7.9	3476	8	ADA43632	Ada43632 Human cDN
147	199.5	12.0	1824	7	ABZ70446	Abz70446 Human CD4	220	131	7.9	3476	8	ADA06894	Ada06894 Human PRO
148	199.5	12.0	2100	5	AAA91011	Aaa91011 Human CD4	221	131	7.9	3476	8	ADA08382	Ada08382 Novel hum
149	199.5	12.0	2100	9	ADD90593	Add90593 Human CD4	222	131	7.9	3476	8	ADB99675	Adb99675 Human PRO
150	199.5	12.0	2307	4	AAO31192	Aao31192 Human epi	223	131	7.9	3476	8	ADB86958	Adb86958 Human PRO
151	199.5	12.0	2308	2	AAQ21186	Aaq21186 Clone CD4	224	131	7.9	3476	8	ADB66113	Adb66113 Human cDN
152	199.5	12.0	2308	2	AAT14725	Aat14725 Human epi	225	131	7.9	3476	9	ADB99791	Adb99791 Human PRO
153	199.5	12.0	2308	2	AAV63462	Aav63462 Human CD4	226	131	7.9	3476	9	ADB99446	Adb99446 Novel hum
154	199.5	12.0	2308	2	AAV81219	Aav81219 Human CD4	227	131	7.9	3476	9	ADB65997	Adb65997 Human cDN

228	131	7.9	3476	9	ADC23395	Adc23395 Human cDN	301	127.5	7.7	1985	7	ACD02956	Novel hum
229	131	7.9	3476	9	ADC26088	Human PRO	302	127.5	7.7	1985	7	ACD01771	Novel hum
230	131	7.9	3476	9	ADE04915	Human PRO	303	127.5	7.7	1985	7	ACA91963	Novel hum
231	131	7.9	3476	9	ADE11221	Human PRO	304	127.5	7.7	1985	7	ACA60174	Human cDN
232	131	7.9	3476	9	ADD88152	Human PRO	305	127.5	7.7	1985	7	ACA89388	cDNA enco
233	131	7.9	3476	9	ADD95447	Human PRO	306	127.5	7.7	1985	7	ACA73398	Human sec
234	131	7.9	3476	9	ADE06377	Human cDN	307	127.5	7.7	1985	7	ACA05713	Human sec
235	131	7.9	3476	9	ADE38152	Human PRO	308	127.5	7.7	1985	7	ACA66547	cDNA enco
236	131	7.9	3476	9	ADD88268	Human PRO	309	127.5	7.7	1985	7	ACD07574	Novel hum
237	131	7.9	3476	9	ADD90849	Human cDN	310	127.5	7.7	1985	7	ACF20122	Human sec
238	131	7.9	3476	10	ADES1702	Ades1702 Human cDN	311	127.5	7.7	1985	7	ACF19508	Human sec
239	131	7.9	3476	10	ADES1818	Human cDN	312	127.5	7.7	1985	7	ACD21796	Human sec
240	131	7.9	3476	10	ADE37676	Human cDN	313	127.5	7.7	1985	7	ACF12961	Human sec
241	131	7.9	3476	10	ADE37560	Human cDN	314	127.5	7.7	1985	7	ACD25064	Human sec
242	131	7.9	3476	10	ADD95331	Adde95331 Human PRO	315	127.5	7.7	1985	7	ACF00113	Human sec
243	131	7.9	3476	10	ADE38031	Human cDN	316	127.5	7.7	1985	7	ACA72170	Human hum
244	131	7.9	3476	10	ADE761120	Ades761120 Human PRO	317	127.5	7.7	1985	7	ACD04694	Novel hum
245	131	7.9	3476	10	ADE39443	Human PRO	318	127.5	7.7	1985	7	ACD18155	Human sec
246	131	7.9	3476	10	ADE304247	Ades04247 Human PRO	319	127.5	7.7	1985	7	ACD08162	Human sec
247	131	7.9	3476	10	ADE39844	Human PRO	320	127.5	7.7	1985	7	ABX71622	Human cDN
248	131	7.9	3476	10	ADE19709	Human PRO	321	127.5	7.7	1985	7	ACA88596	Novel hum
249	131	7.9	3476	10	ADE77287	Ades77287 Human cDN	322	127.5	7.7	1985	7	ACA70038	Human sec
250	131	7.9	3476	10	ADE65395	Ades65395 Human PRO	323	127.5	7.7	1985	7	ACD12260	Novel hum
251	131	7.9	3476	10	ADE76004	Ades76004 Human PRO	324	127.5	7.7	1985	7	ACG74175	Human sec
252	131	7.9	3476	10	ADE37915	Ades37915 Human PRO	325	127.5	7.7	1985	7	ACD15803	Human sec
253	131	7.9	3476	10	ADE64525	Ades64525 Human PRO	326	127.5	7.7	1985	7	ACD25371	Novel hum
254	131	7.9	3476	10	ADE38860	Ades38860 Human PRO	327	127.5	7.7	1985	7	ACD17848	Human sec
255	131	7.9	3476	10	ADE851934	Ades851934 Human cDN	328	127.5	7.7	1985	7	ACC88135	Human sec
256	131	7.9	3476	10	ADD90965	Adde90965 Human cDN	329	127.5	7.7	1985	7	ACD21489	Human sec
257	131	7.9	3476	10	ADE38744	Ades38744 Human PRO	330	127.5	7.7	1985	7	ACD18556	Human sec
258	131	7.9	3476	10	ADE37444	Ades37444 Human cDN	331	127.5	7.7	1985	7	ACH06954	Human sec
259	131	7.9	3476	10	ADE06261	Ades06261 Human cDN	332	127.5	7.7	1985	7	ABX98166	Human cDN
260	131	7.9	3476	10	ADD90120	Adde90120 Human cDN	333	127.5	7.7	1985	7	ACD13917	Human PRO
261	131	7.9	3476	10	ADE38628	Ades38628 Human PRO	334	127.5	7.7	1985	7	ACC09697	Human sec
262	131	7.9	3476	10	ADE39559	Ades39559 Human PRO	335	127.5	7.7	1985	7	ACC88442	Human sec
263	131	7.9	3476	10	ADD89164	Adde89164 Human PRO	336	127.5	7.7	1985	7	ACD21182	Human sec
264	131	7.9	3476	10	ADD88931	Adde88931 Human PRO	337	127.5	7.7	1985	7	ABX77554	Human cDN
265	131	7.9	3476	10	ADE19825	Ades19825 Human PRO	338	127.5	7.7	1985	7	ABX97757	Human PRO
266	131	7.9	3476	10	ADRE77403	Ades77403 Human cDN	339	127.5	7.7	1985	7	ACA97233	Novel hum
267	131	7.9	3476	10	ADE65279	Ades65279 Human PRO	340	127.5	7.7	1985	7	ACA57696	Human PRO
268	131	7.9	3476	10	ADRE65279	Ades65279 Human PRO	341	127.5	7.7	1985	7	ACD14224	Human PRO
269	131	7.9	3476	10	ADRE39327	Ades39327 Human PRO	342	127.5	7.7	1985	7	ACC81452	Human sec
270	130.5	7.9	2652	7	ABZ81728	Abz81728 Rat brain	343	127.5	7.7	1985	7	ACC86412	Human sec
271	130.5	7.9	3077	9	ADB59097	Adb59097 Toxicity-	344	127.5	7.7	1985	7	ACC92849	Human sec
272	130.5	7.9	3681	6	ABL90758	Ab190758 Human pol	345	127.5	7.7	1985	7	ACC91007	Human sec
273	130	7.8	879	8	ACF04000	Acf04000 Human CLE	346	127.5	7.7	1985	7	ACD06946	Human PRO
274	129.5	7.8	1522	3	AAAS7363	Aaa57363 DNA encod	347	127.5	7.7	1985	7	ACC81452	Human sec
275	129.5	7.8	6761	3	AAAS7362	Aaa57362 DNA encod	348	127.5	7.7	1985	7	ACC89056	Human sec
276	128.5	7.8	3259	2	AAT05627	Aat05627 Bovine br	349	127.5	7.7	1985	7	ACC86412	Human sec
277	127.5	7.7	488	8	ACH15082	Ach15082 Human adu	350	127.5	7.7	1985	7	ACC89670	Human sec
278	127.5	7.7	1365	4	AAI58121	Aai58121 Human pol	351	127.5	7.7	1985	7	ACC92849	Human sec
279	127.5	7.7	1984	2	AAAX52252	Aax52252 Protein P	352	127.5	7.7	1985	7	ACA72477	Human PRO
280	127.5	7.7	1984	3	ADC78532	Adc78532 Human PRO	353	127.5	7.7	1985	7	ACA88995	Human sec
281	127.5	7.7	1985	4	AAF72410	Aaf72410 Human PRO	354	127.5	7.7	1985	7	ACA69731	Human sec
282	127.5	7.7	1985	4	AAAS45938	Aas45938 Human DNA	355	127.5	7.7	1985	7	ACA96874	Novel hum
283	127.5	7.7	1985	7	ABX78541	Abx78541 Human PRO	356	127.5	7.7	1985	7	ACA90870	Novel hum
284	127.5	7.7	1985	7	ACA59070	Acas59070 Human PRO	357	127.5	7.7	1985	7	ACA70652	Human sec
285	127.5	7.7	1985	7	ACA75513	Acas75513 Novel hum	358	127.5	7.7	1985	7	ACC86105	Human sec
286	127.5	7.7	1985	7	ACA70993	Acas70993 Human sec	359	127.5	7.7	1985	7	ACC89977	Human sec
287	127.5	7.7	1985	7	ACC87521	Acc87521 Human sec	360	127.5	7.7	1985	7	ACD12585	Human sec
288	127.5	7.7	1985	7	ACC86907	Acc86907 Human sec	361	127.5	7.7	1985	7	ACF19815	Human sec
289	127.5	7.7	1985	7	ACD04080	Acad04080 Human sec	362	127.5	7.7	1985	7	ABX76759	Human PRO
290	127.5	7.7	1985	7	ACA69411	Acas69411 cDNA enco	363	127.5	7.7	1985	7	ABX96191	Human sec
291	127.5	7.7	1985	7	ACA90256	Acas90256 Novel hum	364	127.5	7.7	1985	7	ACA73091	Novel hum
292	127.5	7.7	1985	7	ACA58467	Acas58467 cDNA enco	365	127.5	7.7	1985	7	ACA05512	cDNA enco
293	127.5	7.7	1985	7	ACC89363	Acc89363 Human sec	366	127.5	7.7	1985	7	ACA68634	Novel hum
294	127.5	7.7	1985	7	ACA98154	Acas98154 Novel hum	367	127.5	7.7	1985	7	ACA74478	cDNA enco
295	127.5	7.7	1985	7	ACA93796	Acas93796 Human sec	368	127.5	7.7	1985	7	ACA70345	Human sec
296	127.5	7.7	1985	7	ACD15189	Adc15189 Human sec	369	127.5	7.7	1985	7	ACD14531	Human PRO
297	127.5	7.7	1985	7	ACC08776	Acc08776 Human sec	370	127.5	7.7	1985	7	ACD20179	Human sec
298	127.5	7.7	1985	7	ACC96696	Acc96696 Human sec	371	127.5	7.7	1985	7	ACA68203	Novel hum
299	127.5	7.7	1985	7	ACF15417	Acf15417 Human sec	372	127.5	7.7	1985	7	ABX98668	Novel hum
300	127.5	7.7	1985	7	ACA72784	Human PRO	373	127.5	7.7	1985	7	ACC81145	Human sec

520	127.5	7.7	1985	8	ACF75471	Human	sec	593	127.5	7.7	1985	8	ACF76085	Human	sec
521	127.5	7.7	1985	8	ADA79571	Human	sec	594	127.5	7.7	1985	8	ACF49377	Human	sec
522	127.5	7.7	1985	8	ACF17131	Human	sec	595	127.5	7.7	1985	8	ACF43834	Human	sec
523	127.5	7.7	1985	8	ACF22885	Human	sec	596	127.5	7.7	1985	8	ACH06179	cdNA	enco
524	127.5	7.7	1985	8	ACF07885	Human	sec	597	127.5	7.7	1985	8	ACH06486	cdNA	enco
525	127.5	7.7	1985	8	ACF08192	Human	sec	598	127.5	7.7	1985	8	ADA83096	Human	sec
526	127.5	7.7	1985	8	ACF40496	Human	sec	599	127.5	7.7	1985	8	ACC92542	Human	sec
527	127.5	7.7	1985	8	ACF53675	Human	sec	600	127.5	7.7	1985	8	ACC93156	Human	sec
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Search completed: August 17, 2004, 02:42:56
Job time : 504 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 16, 2004, 23:14:48 ; Search time 3044 Seconds
(without alignments)
3158.877 Million cell updates/sec

Title: US-10-063-670-6
Perfect score: 1657
Sequence: 1 MARCFSLVLLTSTWTRLL.....NPESKSPKTTVRCLEAEV 322

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=EST -QFMT=FASTAP -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10063670 @CN 1.1 3437 @runat 10082004 165353 13632 -NCPV=6 -ICPV=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database :
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29: gb_gss2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	1476.5	89.1	1201	9	AL546669
5	1439	86.8	1201	9	AL551020
6	1323.5	79.9	1014	9	AL553858
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ALIGNMENTS

RESULT 1
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DEFINITION clone CS0DI039YJ06 5-PRIME, mRNA sequence.
ACCESSION AL550279
VERSION AL550279.2 GI:31272096
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1154)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12887098.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5952.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSODI039DE03QPI&cluster=5952.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSODI039DE03QPI.

FEATURES

source
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 /note="1st strand cDNA was primed with a NotI-oligo (dr)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 9.19e-143 Length: 1154
 Score: 1657.00 Matches: 322
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-063-670-6 (1-322) x AL550279 (1-1154)

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 DB 122 ATGCCAGGCTTTTCAGCTGGTGGTCTCTCTCACTTCCATCTGGACACAGAGCTCCTG 181
 QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
 DB 182 GTCCAGGCTTTTCGTGTCAGAGAGCTTTCCATCAGGTGTCATGAGAAATATGGGG 241
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
 DB 242 ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTCACAGAACTAAGAGGCC 301
 QY 61 CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
 DB 302 TGTAGGCTGTGGGACTAAGTTTGGCGGCAAGACCAAGTTGAACAGAGCTTGAAGACT 361
 QY 81 SerPheGluThrCysSerTyrglyTyrValGlyAspGlyPheValValIleSerArgIle 100
 DB 362 AGCTTTGAACACTTGACGCTATGGCTGGTGGAGATGGATTCGTGTCATCTCAGATT 421
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuLeuThrLysValProVal 120
 DB 422 AGCCCAAAACCCCAAGTGTGGGAAAATGGGGTGGTCTCTGATTGGAAGGTTCCAGTG 481
 QY 121 SerArgGlnPheAlaAlaTyrcysTyrcysSerSerSerAspThrThrAsnSerCysIle 140
 DB 482 AGCCGACAGTTTGAGGCTATTGTATCAACTCTCATCTGGACTTAATCTCGTGATT 541
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
 DB 542 CCAGAAATTATCACCAAGATCCCATATTCACACTCAAACTGCAACACAAACA 601
 QY 161 GluPheIleValSerAspSerThrTyrcysValAlaSerProTyrcysThrIleProAla 180

DB 602 GAATTATTGTCAGTGACAGTACCTACTCGTGGATCCCTTACTTCAATACTGCTGCC 661
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuLeu 200
 DB 662 CCTACTACTACTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATGATT 721
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
 DB 722 TGTGTCAAGAAGTTTTTATGAAACTAGCACCATGCTACAGAACTGAACATTGTT 781
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
 DB 782 GAAATAAAGCAGCATTCAGAAATGAAGCTCTGGTTTGGAGGTGTCCTCCACGGCTCTG 841
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrcysVal 260
 DB 842 CTAGTGTCTGTCTCTCTCTCTTTTGGTGTCTGAGTGTCTTGGATTTCGTATGCTCAA 901
 QY 261 ArgTyrcysValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
 DB 902 AGGTATGTGAAGGCTTCTCTCTTTTCAACAAAGAAATCAGCAGAGAAATGATCGAAACC 961
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
 DB 962 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1021
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
 DB 1022 GATAAAACCCAGAGAGTCCAGAGTCCAGCAAAACTACCGTSCGATGCTGGAAGCT 1081
 QY 321 GluVal 322
 DB 1082 GAAGTT 1087

RESULT 2
 AL550621 1201 bp mRNA linear EST 31-MAY-2003
 LOCUS AL550621 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CSODI058YN14 5-PRIME, mRNA sequence.

ACCESSION AL550621
VERSION AL550621.2 GI:31272438
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)
 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:12887768.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5952.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSODI058DG07QPI&cluster=5952.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSODI058DG07QPI.

FEATURES
 Location/Qualifiers
 1. .1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODI058YN14"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dr)"

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

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Alignment Scores:
Pred. No.:      3,64e-129      Length:      1201
Score:          1510.50      Matches:      296
Percent Similarity: 95.53%      Conservative: 3
Best Local Similarity: 94.57%      Mismatches: 11
Query Match: 91.16%      Indels: 3
DB: 9      Gaps: 1

US-10-063-670-6 (1-322) x AL550621 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 158 ATGGCCAGGTGCTTCAGCCTGGTGTCTCTCCTCCTCCATCTGGACCCAGAGCTCCTG 217
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 218 GTCCAAAGGCTCTTTGGTGCAGAAAGACTTTCATCCAGGTGTCATGCAAAATTATGGGG 277
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 278 ATCACCCCTGTGAGCAAAAGGCAACAGCAGCTGAAATTCACAGAGCTAAGGAGGCC 337
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 338 TGTAGGCTGCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 397
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 398 AGCTTTGAACTTGCAGCATGCTGGTGGAGATGGATTCGTGTCATCTAGGATT 457
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValIleLeuTrpLysValProVal 120
Db 458 AGCCCAAAACCCCAAGTGTGGGAAATGGGTGGGTGCTCTGATTTGGAGGTTCCAGTG 517
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 518 AGCCGACAGTTTGCAGCTATTGTTCAACTCATCTCATCTGATCTGGACTAATCGTGCAAT 577
QY 141 ProGluIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 578 CCAAGAAATATACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAA 637
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 638 AAATTTATTGTCAGTGACAGTACTACTCGTGGCATCCCTTACTCTACATACCTGCC 697
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 698 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTTGATT 757
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 758 TGTGTCACAGAGATTTTATGGAAACTAGCACCATGTCATACAGAAACTGAACATTGTT 817
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 818 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGTGTCCCCACGGCTCTG 877
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 878 CTAGTGCTTCTCTCTCTCTTTTGGTGTGTCAGCTGCTCTTGGATTTTGTCTATGTCAA 937
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 938 AGTATGTGAAGCCCTTCCCTTTTACAAAWAAATAATCAGCMGAGGAAATGTGCGADACC 997
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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Db 998 MAAGTAGTAAGGAGGAGAGGCAATGATWASCAACCCYAAATGAGGATCAAAAGAAACT 1057
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThr 313
Db 1058 GWTAATAACCCG-----AAGAGTCCAGAGTCMAGC 1087

RESULT 3
AL552299 Homo sapiens 1015 bp mRNA linear EST 31-MAY-2003
LOCUS clone CS0D1069YN02 5-PRIME, mRNA sequence.
DEFINITION AL552299
ACCESSION AL552299
VERSION AL552299.2 GI:31274114
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1015)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12891068.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1069D01Q1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0D1069D01Q1.

FEATURES
Location/Qualifiers
1..1015
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1069YN02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.:      1.9e-126      Length:      1015
Score:          1480.00      Matches:      288
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 89.32%      Indels: 0
DB: 9      Gaps: 0

US-10-063-670-6 (1-322) x AL552299 (1-1015)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 144 ATGGCCAGGTGCTTCAGCCTGGTGTCTCTCCTCCTCCATCTGGACCCAGAGCTCCTG 203
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 204 GTCCAAAGGCTCTTTGGTGCAGAAAGACTTTCATCCAGGTGTCATGCAAAATTATGGGG 263
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 264 ATCACCCCTGTGAGCAAAAGGCAACAGCAGCTGAAATTCACAGAGCTAAGGAGGCC 323
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Db 324 TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACAGCGCTTGAAGACT 383
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile 100
Db 384 AGCTTTGAAACTTGACGCTATGGCTGGGTGGAGATGGATTGGTGGTCATCTCAGGATT 443
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 444 AGCCCAACCCCAAGTGTGGGAAAATGGGGTGGGTGCTGATTTGGAAGGTTCCAGTG 503
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysile 140
Db 504 AGCCGACAGTTTGCAGCTATTGTTTACAACTCATCTGATCTGACCTAACTCGTGCAAT 563
Qy 141 ProGluIleIleThrLysAspProIlePheAsnThrGlnThrAlaThrGluThrThr 160
Db 564 CCAGAAATATACACCAAGATGCCATATTCACACTCAAACTGCAACCAACAACA 623
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 624 GAATTTATGTCAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAAATACCTGCC 683
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeulle 200
Db 684 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 743
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 744 TGTGTACAGAAAGTTTATGGAACTAGCACCATGCTCTACAGAACTGAACCAATTGTT 803
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 804 GAAATAAAGCAGCATTCAGAAATGAAGTCTCTGGGTTTGGAGGTGTCCTCCACGCTCTG 863
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 864 CTAGTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 923
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 924 AGGTATGTGAAGGCTTCCCTTTTACAAAGAAATCAGCAAGAAATGATCGAAACC 983
Qy 281 LysValValLysGluGluLysAla 288
Db 984 AAGTAGTAAAGGAGGAGAGGCC 1007
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RESULT 4

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AL546669
LOCUS
DEFINITION AL546669 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI029YJ09 5-PRIME, mRNA sequence.
ACCESSION AL546669
VERSION AL546669.2 GI:31268502
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12880008.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI029CE05QPI&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
```

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI029CE05QPI.

FEATURES
source

1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI029YJ09"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dtr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

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Alignment Scores:
Pred. No.: 5,13e-126 Length: 1201
Score: 1476.50 Matches: 302
Percent Similarity: 96.24% Conservative: 5
Best Local Similarity: 94.67% Mismatches: 11
Query Match: 89.11% Indels: 5
DB: 9 Gaps: 1

US-10-063-670-6 (1-322) x AL546669 (1-1201)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 126 ATGCCCAAGGCTTCAGCGTGGTGTCTTCTCATCTCCATCTGCACCGAGGCTCTCTG 185
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgileMetGly 40
Db 186 GTCCAGGCTCTTTGGTGGTGAGAGAGCTTTCATCCAGGTTGTCATGCAGAAATATATG 245
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 246 ATCACTCTGTGAGCAAAAGGCGAAGCAGCAGCTGAATTTTCACAGAAAGCTTAAGG 305
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 306 TGTAGGCTGTGGGACATAAGTTTGGCCGGCAGGACCAAGTTGAACAGCTTGAAGCT 365
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile 100
Db 366 AGCTTTGAACTTGACGCTATGGCTGGGTGGAGATGGATTTCGGTGTCATCTCAGGATT 425
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 426 AGCCCAACCCCAAGTGTGGGAAAATGGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 485
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysile 140
Db 486 AGCCGACAGTTTGCAGCTATTGTTTACACTCACTCTGACTTGGACTTAATCTGTGCAAT 545
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 546 CCAGAAATATACACCAAGATGCCATATTCACACTCAAACTGCAACCAACAACA 605
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 606 GAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 665
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeulle 200
Db 666 CTTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 725
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 726 TGTGTACAGAAAGTTTATGGAACCTAGCACCATGCTCTACAGAACTGAACCACTTGT 785
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 786 GAAATAAAGCAGCATTCAGAAATGAAGCTCTGGGTTTGGAGGTGTCTCCACGCTCTG 845
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QY 241 LeuValLeuAlaLeuLeuPheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
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 Db 846 CTAGTCTGCTCTCTCTCTCTTTGGTGGCGAGCTGCTGGATTTGCTATGCAAA 905
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 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
 |||||
 Db 906 AGGTATGTGAAGCCCTTCCCTTTTACAACAAGAAATCAGAGAGGAATGATCGAAACC 965
 |||||
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300
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 Db 966 ACAGTAGTAGAAGAGGR-GAGGGCAATGATAGCAM-CCTAATGGGATC--AAAGAAACT 1021
 |||||
 QY 301 AspLysAsnProGluGluSerLysThrProSerLysThrValArgCysLeuGlu 319
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 Db 1022 GATAAAAA-CCAGAGAGTCCAGA---GTCCAGCAAACTTMCGTGCGATCTCGGAG 1074
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RESULT 5
 AL551020
 LOCUS
 DEFINITION AL551020 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1066YJ13 5-PRIME, mRNA sequence.
 AL551020
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:12888564.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5952.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1066CF07QPL&cluster=5952.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D1066CF07QPL.
 Location/Qualifiers
 1. .1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1066YJ13"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
 source
 1. .1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1066YJ13"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

Alignment Scores:
 Pred. No.: 1-53e-122 Length: 1201
 Score: 1439.00 Matches: 300
 Percent Similarity: 94.98% Conservative: 3
 Best Local Similarity: 94.04% Mismatches: 14
 Query Match: 86.84% Indels: 7
 DB: 9 Gaps: 2

US-10-063-670-6 (1-322) x AL551020 (1-1201)
 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIlePheThrArgLeuLeu 20
 |||||
 Db 98 ATGGCCAGGTGCTTCAGCTGGTGGTGGTCTCTCATTCCATCTGGACCGAGGCTCTG 157
 |||||

QY 21 valGlnGlySerLeuThrGAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
 |||||
 Db 158 GTCCAAAGGCTCTTTGGTGGCGAGAGCTTTCATCCAGGTGTTCATGCAGAAATATGGGG 217
 |||||
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
 |||||
 Db 218 ATCACCCCTTGTGAGCAAAAGGCAACCCAGCAGCTGAATTTTCAGAAGCTAAGGAGGCC 277
 |||||
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
 |||||
 Db 278 TGTAGGCTGCTGGGACTAAGTTTGGCGCGCAAGCAAGTTGAAACAGCCTTGAAAGCT 337
 |||||
 QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValLysSerArgIle 100
 |||||
 Db 338 AGCTTTGAACCTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGTCATCTCTAGGATT 397
 |||||
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
 |||||
 Db 398 AGCCCAAAACCCAGTGTGGGAAAAAATGGGTGGGTGCTGCTGATTTGGAGGTTCAGTG 457
 |||||
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
 |||||
 Db 458 AGCCGACAGTTTGCAGCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTCAATT 517
 |||||
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
 |||||
 Db 518 CCAGAAATTTATCCACCACCAAGATCCCATATTTCAACACTCAAACTCAACACACAAACA 577
 |||||
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
 |||||
 Db 578 GAATTTATTTGTGAGTGACAGTACTTCTGGTGGCATCCCTTACTCTCAATACCTGCC 637
 |||||
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
 |||||
 Db 638 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATT 697
 |||||
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
 |||||
 Db 698 TGTGTCCACAGAGATTTTTATGGAACCTAGCACCATCTGTACAGAAACTGAACCATTTGTT 757
 |||||
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
 |||||
 Db 758 GAAATTAAGCAGCATTCAGAAATGAAGCTGTGGGTGGGTGGGTGTCCCGCGCTCTG 817
 |||||
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
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 Db 818 CTAGTGTCTTCTCTCTCTCTTTTGGTGTGTGTCAGCTGGTCTTGGATTTTGTATGTCAAA 877
 |||||
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
 |||||
 Db 878 AGGTATGTGAAGGC-TTCCCTTTTACAAACAAGATCAGCAGAGAAATGATCGAAACC 936
 |||||
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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 Db 937 AGATA-GTAAAGGCGAGAGGCGC-AATGATAGCAA-CCTAATGAGGA-TCAAAGAAACT 992
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 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGlu 319
 |||||
 Db 993 GATAAAACC---AGAAGAGTCAAGAGTCCAGCAAACTACGKG---CGATGCTKGCAG 1043
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RESULT 6
 AL553858
 LOCUS
 DEFINITION AL553858 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1077YJ17 5-PRIME, mRNA sequence.
 AL553858
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1014 bp mRNA linear EST 31-MAY-2003

```

REFERENCE
1 (bases 1 to 1014)
Li W.B., Gruber C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
COMMENT
On Feb 15, 2001 this sequence version replaced gi:12894087.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1077CE09QPl&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1077CE09QPl.

FEATURES
source
1..1014
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1077J17"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (drr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 5,96e-112 Length: 1014
Score: 1323.50 Matches: 272
Percent Similarity: 98.55% Conservative: 0
Best Local Similarity: 98.55% Mismatches: 4
Query Match: 79.87% Indels: 4
DB: 9 Gaps: 0

US-10-063-670-6 (1-322) x ALU553858 (1-1014)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db 162 ATGGCAGGCTGTTTCAGCGTGGTGTGTTCTCACTTCATCTGCACACGAGGCTCTG 221
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 222 GTCCAAGGCTCTTTGCGTGCAAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 281
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 282 ATCACTTTGTGACAAAAGCGAACCCAGCAGCTGATTTTCACAGAGCTTAAGAGGCC 341
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 342 TGTAGGCTGCTGGGCAATAGTTTGGCCGCGCAAGACCAAGTTGAACAGCCTTCAAGCT 401
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 402 AGCTTTGAACCTTCAGCTATGGCTGGGTTGGAGATGATTCGTTGATCTCTAGGATT 461
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 462 AGCCCAACCCCAAGCTGTGGGAAAAATGGGTGGGTGGGTGGTGGTGGTGGTGGTGGTGGT 521
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 522 AGCCGACAGTTTGCAGCCTATTGTTTACAACTCATCTGATCTGACTTAACCTCGGCATT 581
Qy 141 ProGluIleLeuThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 582 CCAGAAATTTATCACCACCAAGATCCCATATTTCAACACTCAACACTGCACACCAACA 641

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Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 642 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 701
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeu 200
Db 702 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAATTGATT 761
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 762 TGTGTCAAGAAGTTTATTGAAACATGACACCATGCTACAGAACTGAACCACTTTGTT 821
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 822 GAAATAAAGCAGCATTTCAAGATGAAGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 880
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLysGlyPheCysTyrValLys 260
Db 881 CTAGTGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGlu 276
Db 940 AGGTATGTGAAGGCTT-CCYTTTACAACAR-AATCAGCAGAGAGAA 984

RESULT 7
BX459046 913 bp mRNA linear EST 22-MAY-2003
LOCUS BX459046 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0D011YN20
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX459046
VERSION BX459046.1 GI:31021086
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 913)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D011DG10QPl&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D011DG10QPl.

FEATURES
source
1..913
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D011YN20"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo (drr) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Alignment Scores:
Pred. No.: 2,53e-111 Length: 913
Score: 1316.00 Matches: 260
Percent Similarity: 99.62% Conservative: 0
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 79.42% Indels: 1

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DB: 13 Gaps: 0
US-10-063-670-6 (1-322) x BX459046 (1-913)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 132 ATGCCAGGTCCTTACGCTGGTGTCTCTCTACATTCCTGACACGAGGCTCTCTG 191
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 192 GTCCAGAGGCTCTTGGCTGCAGAGAGCTTCCATCCAGGTGTCTATCAGAAATATGGG 251
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 252 ATACCCCTTGTGAGCAAAAGGGAACACAGCTGATTTTCAGAGCTATAGGAGGCC 311
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 312 TGTAGGCTGCTGGGACTAAGTTTGGCGGCAAGACCAAGTTGAAACAGGCTTGAAAGCT 371
QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db 372 AGCTTTGAACTTTCAGCTATGCTGGTTTGGAGATGATTCGTGTCATCTCTAGGATT 431
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 432 AGCCCAACCCCAAGTGTGGGAAATATGGGTGGGTGCTCTGATTTGGAAGTTCCAGTG 491
QY 121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 492 AGCCGACAGTTTTCAGCTTATTTGTAACAATCTATCTGATCTGAGCTTGAAGCTTGC 551
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 552 CCAGAAATATATACCAACCAAGATCCCATATTAACACTCAAACTCAACACAAACAACA 611
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 612 GAATTTATTTGTCAGTGACAGTACTACTCGTGGCATCCCTTACTCTACAAATACCTGCC 671
QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 672 CCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 731
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrThrGluThrGluProPheVal 220
Db 732 TGTGTACAGAGATTTTATGGAAACTAGCACCATCTGTACAGAAACTGAACCATTTGTT 791
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 792 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTGGAGGTGT-CCACGGCTCTG 850
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 851 CTAGTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 910
QY 261 Arg 261
Db 911 AGG 913

RESULT 8
BX366718 1201 bp mRNA linear EST 08-MAY-2003
LOCUS BX366718 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1040YD03 5-PRIME, mRNA sequence.
ACCESSION BX366718
VERSION BX366718.1 GI:30451557
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)

```

AUTHORS TITLE JOURNAL COMMENT

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0A1040CB02QP1&cluster=5952.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0A1040CB02QP1.

FEATURES

source

1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1040YD03"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoK V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 4,33e-108 Length: 1201
Score: 1283.00 Matches: 260
Percent Similarity: 94.89% Conservative: 0
Best Local Similarity: 94.89% Mismatches: 14
Query Match: 77.43% Indels: 2
DB: 13 Gaps: 0
US-10-063-670-6 (1-322) x BX366718 (1-1201)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 212 ATGCCAGGTCCTTACGCTGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 271
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 272 GTCCAGAGGCTCTTGGCTGCAGAGAGCTTCCATCCAGGTGTCTATCAGAAATATGGG 331
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 332 ATCACCTTGTGAGCAAAAGGCAACACGACGCTGAATTTACAGAAGCTAAGGAGGCC 391
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 392 TGTAGGCTGCTGGACTAAGTTTGGCGGCAAGACCAAGTTGAAACAGCTTGAAGCT 451
QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db 452 AGCTTTGAAACTTTCAGCTATGCTGGTTGGAGATGGATTCGTGTCATCTCTAGGATT 511
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 512 AGCCCAACCCCAAGTGTGGGAAATATGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 571
QY 121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 572 AGCCGACAGTTTTCAGCTTATTTGTAACAATCTATCTGATCTGAGCTAATCTGTCATT 631
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 632 CCAGAAATATATACCAACCAAGATCCCATATTAACACTCAAACTCAACACAAACAACA 691
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

692	GAATTTANTGTCACTGACAGTACCTACTCGGTGGGATCCCTTACTCTACAAATACCTGCC	751
181	ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
752	CCTACTACTACTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	811
201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
812	TGTGTGCAGAGAAGTTTTATGGAACATAGACCATTGCTACAGAAACTGGAACCAATTGTT	871
221	GluAsnLysAlaAlaPheLysAsnGluAlaalaGlyPheGlyGlyValProThrAlaLeu	240
872	GAAAAATAAGCAGCATTWAAGAAATKAAGCTCTGGGTTTGG- AKGTKTCCCAKCGCTCTG	930
241	LeuValLeuAlaLeuLeuPhePheGlyAlaalaGlyLeuGlyPheCysTyrValLys	260
931	CTAGTGTCTTCTCTCTCTCTCTTTGGTGTCTCAGCTGCTGTGKATTTTTKCTATGTCAAC	990
261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGln	274
991	ADGPTATCTGAAGGCAC- CCTTTTTCACMAGAATCAGCAG	1031

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RESULT 9
AL550911
LOCUS
DEFINITION
AL550911 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI065VD17 5-PRIME, mRNA sequence.
1172 bp mRNA linear EST 31-MAY-2003

ACCESSION
AL550911
VERSION
AL550911.2
KEYWORDS
GI:31272728
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1172)
Li, W.B.; Gruber, C.; Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
On Feb 15, 2001 this sequence version replaced gi:12888352.
COMMENT

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FEATURES source

ORIGIN

Alignment Scores:

Alignment Scores:			
Pred. No.:	1.21e-107	Length:	1172
Score:	1278.00	Matches:	277
Percent Similarity:	91.25%	Conservative:	6
Best Local Similarity:	89.33%	Mismatches:	24
Query Match:	77.13%	Indels:	9
DB:	9	Gaps:	2

US-10-063-670-6 (1-322) x AL550911 (1-1172)

Qy	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	154	ATGGCCAGGTGCTTACGCTGGTGTGCTTCTSACTTSCATCTGGACACAGAGGTCCTG	213
Qy	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	214	GTCCAAGGCTCTTTGGTGCAAGAAGCTTTCATCCAGGTGTCATGSAAGATATGGGG	273
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	274	ATGACCCCTTGTGAGCAAAAGGGAASCACGACGCTGAATTTASAGAAGCTAAGGAGGCC	333
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	334	TGTAGGCTGTGGGACTTAAGTTTGGCGCGGCAAGGACCAAGTTGAAACAGCCCTTGAAGCT	393
Qy	81	SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle	100
Db	394	AGCTTTGAAACTTTCAGCTATGSGTGGTGGAGATGGATTSGTGGTCATCTCTAGGATT	453
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValleulleTrpLysValProVal	120
Db	454	AGSCAAACSCCAAGTGTGGGAAAAATGGGGTGGGTGTSCTGAATTTGGAAGGTTCCAGTG	513
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	514	AGCSGACAGTTTGCAGCCTATTGTTCAACTCATCTGATCTTGGACTACTCGTGCAATT	573
Qy	141	ProGluIleIleThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	574	SSAGAAATTATACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACAACA	633
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThr-IleProAl	180
Db	634	GAATTTATTGTCAGTGACAGTACTCTCGGTGGCATCCCTTACTCTACGAATACCTGS	693
Qy	180	aProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuI	200
Db	694	SCCTACTACT	753
Qy	200	eCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVa	220
Db	754	TTGTGTSACAGAAGTTTTTATGAAACTAGCACCATGTCTACAAACCACTGAACCATTTGT	813
Qy	220	LGlusAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLe	240
Db	814	TGAATTAAGCAGCATTTCAAGATGAAGCTGCTGGTTGGAGGTGT-CCCACGGCTCT	872
Qy	240	uLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVally	260
Db	873	GCTAGTCTTCT	932
Qy	260	sArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluTh	280
Db	933	AAGGTATGTGAAGGCSCTTCCTTTTACAAACAGCAT-CAGCAAGAAGA-ATGATCGAAAC	990
Qy	280	rLysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysTh	300
Db	991	CAAGTA-GTAAAGGAGAGAGGC--AATGATAGCAC-CCTTAATGAGGAT--CAAGAAC	1043
Qy	300	rAspLysAsnProGluGluSerLysSer	309
Db	1044	TGACAAAWMC---MGAAGRTCAAARTCA	1068

RESULT 10
 LOCUS AL549512
 DEFINITION AL549512 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSOD1044YN16 5-PRIME, mRNA sequence.
 ACCESSION AL549512
 VERSION AL549512.2 GI:31271330

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KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM

REFERENCE
1 (bases 1 to 972)
AUTHORS     Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12885569.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI044DG08QPI&cluster=5952.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI044DG08QPI.

FEATURES
source
1..972
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DI044YN16"
    /tissue_type="PLACENTA COT 25-NORMALIZED"
    /note="1st strand cDNA was primed with a NotI-oligo(dT)
    primer. Five prime end enriched, double-strand cDNA was
    digested with Not I and cloned into the Not I and EcoR V
    sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.:      1..74e-107      Length:      972
Score:          1275.00          Matches:     261
Percent Similarity: 96.36%      Conservative: 4
Best Local Similarity: 94.91%   Mismatches: 9
Query Match:     76.95%        Indels:      4
DB:              9             Gaps:        1

US-10-063-670-6 (1-322) x AL549512 (1-972)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db      143 ATGCCAGGCTTCAGCCTGGTGTCTTCTCATTCCATCTGGACACAGAGCTCCTG 202
QY      21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      203 GTCCAAAGGCTCTTTGGCTGCAGAAAGAGCTTCCATCCAGGTGCATGCAGAAATTATGGGG 262
QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      263 ATCAACCTTGAGCAAAAGGCGAACACGACGACTGATTTTCAGAGCAAGAGAGGCC 322
QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      323 TGTAGGCTGCTGGGACTAAGCTTTGGCGCGCAAGACCAAGCTTGAAACAGCCTTGAAAGCY 382
QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db      383 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTGCATCTCTAGGATT 442
QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      443 AGCCCAACCCCAAGTGTGGGAAAATGGGGTGGGTCTCTGATTGGAAAGGTTCCAGTG 502
QY      121 SerArgGlnPheAlaLysTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      503 AGCCGACAGTTTGCAGGCTATTGTTACAACTCATCTGATCTTGGACTACTCTGTCGATT 562

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QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      563 CCAGAAATATATACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 622
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      623 GAATTTATTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 682
QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeu 200
Db      683 CCTACTACTACTCTCTCTCTCCAGCTTCACATCTCTATTCACGCGAGAAAAAATTGATT 742
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      743 TGTGTACAGAAAGTTTATTATGGAATAGCACCATGCTACAGAAACTGAACATTGTT 802
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db      803 GAAATTAAGCAGCATTCAGAAATGAAGCTGCTGGGTTGGAGGTGTCCTCCMCG-GCTCTK 861
QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      862 CTAGTCTTKCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 919
QY      261 ActGlyValLysAlaPheProPheThrAsnLysAsnGlnGlnLys 275
Db      920 AGGTATGTAGGSGCT--TCCTTTTCAAWAAGATAAASAGAAGG 961

RESULT 11
AL543874
LOCUS    AL543874 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION
ACCESSION AL543874
VERSION    AL543874.2 GI:31265719
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 911)
AUTHORS   Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:12876353.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI005AD07QPI&cluster=5952.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI005AD07QPI.

FEATURES
source
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    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DI005YG13"
    /tissue_type="PLACENTA COT 25-NORMALIZED"
    /note="1st strand cDNA was primed with a NotI-oligo(dT)
    primer. Five prime end enriched, double-strand cDNA was
    digested with Not I and cloned into the Not I and EcoR V
    sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:

```

```

Pred. No.: 1.65e-106 Length: 911
Score: 1264.00 Matches: 251
Percent Similarity: 99.60% Conservative: 0
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 76.28% Indels: 1
DB: 9 Gaps: 0

US-10-063-670-6 (1-322) x AL543874 (1-911)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleThrThrArgLeuLeu 20
Db 155 ATGCCCGAGGCTCTTTCAGCTGGTGTGCTTCTCACTTCACATCGACACAGGCTCTG 214
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 215 GTCCAGGCTCTTTCGCGTCAGAGAGCTTTCCATCCAGGTGTATGACAGAAATATGGGG 274
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 275 ATCACCTTGTGAGCAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 334
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 335 TGTAGGCTGTGGGACTTAAGTTTGGCGGCAAGGACCAAGTTGAACAGCCTTGAAAGCT 394
Qy 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db 395 AGCTTTGAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCACTCTTAGGATT 454
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleThrLysValProVal 120
Db 455 AGCCCAAAACCCAAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 514
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrThrThrAsnSerCysIle 140
Db 515 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGTACTTGGACTTAATCTCGTCATT 574
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 575 CCAGAAATTATCACCAACCAAGATCCCATATTCACACTCAACTCAACATGCAACCAACA 634
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 635 GAATTTATTGTTCAGTACAGTACCTTACTCGGTGGCATCCCTTACTCTCAATAACCTGCC 694
Qy 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 695 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 754
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 755 TGTGTACAGAAATTTTATGGAACCTAGCACCATGCTCTACAGAACTGACCATTTGTT 814
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 815 GAAATAAAGCAGCATTCACAAATGAAGCTGCTGGTTTGGAGGTGT-CCCAACGCTCTG 873
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAla 252
Db 874 CTAGTGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 909

RESULT 12
AL547774
LOCUS
DEFINITION AL547774 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1033YD11 5-PRIME, mRNA sequence.
ACCESSION AL547774
VERSION AL547774.2 GI:31269603
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

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REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12882152.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1033CB06QPl&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1033CB06QPl.
FEATURES
Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1033YD11"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/note="First strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 3.81e-106 Length: 1201
Score: 1262.00 Matches: 262
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 95.27% Mismatches: 10
Query Match: 76.16% Indels: 5
DB: 9 Gaps: 1
US-10-063-670-6 (1-322) x AL547774 (1-1201)
Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleThrThrArgLeuLeu 20
Db 263 ATGCCCGAGGCTCTTTCAGCTGGTGTGCTTCTCACTTCACATCGACACAGGCTCTG 322
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 323 GTCCAAGGCTCTTTCGCGTCAGAGAGCTTTCCATCCAGGTGTATGCAAAATATATGGGG 382
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 383 ATCACCTTGTGAGCAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 442
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 443 TGTAGGCTGTCTGGACTTAAGTTTGGCGGCAAGGACCAAGTTGAACAGCCTTGAAAGCT 502
Qy 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db 503 AGCTTTGAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCACTCTTAGGATT 562
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleThrLysValProVal 120
Db 563 AGCCCAAAACCCAAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 622
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrThrThrAsnSerCysIle 140
Db 623 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGTACTTGGACTTAATCTCGTCATT 682
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 683 CCAGAAATTATCACCAACCAAGATCCCATATTCACACTCAACTCAACATGCAACCAACA 742

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QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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 Db 743 GAATTTATTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTCAATAACCTGCC 802
 |||||
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuile 200
 |||||
 Db 803 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATT 862
 |||||
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
 |||||
 Db 863 TGIGTCACAGAGTTTTATGGAAATAGCAGCATGCTACAGAACTGAACCATTTGTT 922
 |||||
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
 |||||
 Db 923 GAAATAAAGCAGCAITTCAGAAATGAGCTGCTGGGTTTGAGAGTGCTCCCMCG-GCTCTG 981
 |||||
 QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
 |||||
 Db 982 CTAGTGTCT 1039
 |||||
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLys 275
 |||||
 Db 1040 RG-TATGTGAGSCT---CCCTTTTCAAMARAATMRCAGAGG 1080
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RESULT 13
 AL552127 1172 bp mRNA linear EST 31-MAY-2003
 LOCUS
 DEFINITION
 AL552127 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0DI059YA12 5-PRIME, mRNA sequence.

ACCESSION
 AL552127
 VERSION
 AL552127.2 GI:31273943
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1172)
 Li, W.B., Gruber, C., Jessee, J. and Polaves, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)

COMMENT
 On Feb 15, 2001 this sequence version replaced gi:12890728.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 Bp 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5952.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DI059BA06QPl&cluster=5952.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DI059BA06QPl.

FEATURES
 source
 1. .1172
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI059YA12"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /notes="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 2,51e-105 Length: 1172
 Score: 1253.00 Matches: 259
 Percent Similarity: 95.94% Conservative: 2
 Best Local Similarity: 95.20% Mismatches: 10
 Query Match: 75.62% Indels: 4

RESULT 14

BX402505

LOCUS

DEFINITION

BX402505

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 1201)

DB: 9 Gaps: 1

US-10-063-670-6 (1-322) x AL552127 (1-1172)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
 |||||
 Db 242 ATGGCCAGGTCCTTACGCTGGTGTGTTCTTCTCATTCCATCTGGACCCACGAGGCTCTG 301
 |||||

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
 |||||
 Db 302 GTCACAGGCTCTTTTGGCTGCAGAAAGCTTTCCATCCAGGTGTCAAGCAGAAATATGGG 361
 |||||

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
 |||||
 Db 362 ATCACCTTGTGAGCAAAAGGCAACCGACGACTGAATTTTACAGAAAGCTAAGGAGGCC 421
 |||||

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
 |||||
 Db 422 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTTGAAGCT 481
 |||||

QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
 |||||
 Db 482 AGCTTTGAAACTTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTGTCATCTCTAGGAT 541
 |||||

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValIleLeuThrLysValProVal 120
 |||||
 Db 542 AGCCCAAAACCCAGTGTGGGAAAATGGGTGGGTCTCTGATTTGGAGAGGTTCAGTG 601
 |||||

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrThrTrpThrAsnSerCysIle 140
 |||||
 Db 602 AGCCGACAGTTTGCAGCTTGTGTTTCAACTCATCTGATCTGGACTTAACCTGTCAT 661
 |||||

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
 |||||
 Db 662 CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCACACAAACA 721
 |||||

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
 |||||
 Db 722 GAATTTATTGTGAGTACAGTACTACTCGGTGGCATCCCTTACTCTCAATACCTGCC 781
 |||||

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuile 200
 |||||
 Db 782 CCTACTACTACT 841
 |||||

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
 |||||
 Db 842 TGTGTACAGAAATTTTATGAAACTAGCACCATCTGTACAGAAACTGAACA-TTTGTT 900
 |||||

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
 |||||
 Db 901 GA-ATAAAGCGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCGGCTCTT 959
 |||||

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
 |||||
 Db 960 CTAGTGTCTGCT 1018
 |||||

QY 261 ArgTyrValLysAlaPheProPheThrAsnLys 271
 |||||
 Db 1019 RGTATTTTAAGG---CTTCCCTTTTAYAAACAAA 1048
 |||||

BOX402505 1201 bp mRNA linear EST 13-MAY-2003
 BX402505 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0DI045YA10 5-PRIME, mRNA sequence.

ACCESSION
 BX402505
 VERSION
 BX402505.1 GI:30630733
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5952.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS1A1012ZA06QPl&cluster=5952.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS1A1012ZA06QPl.

FEATURES
 source
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODI045A10"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Alignment Scores:
 Pred. No.: 1.97e-104 Length: 1201
 Score: 1243.50 Matches: 259
 Percent Similarity: 97.74% Conservative: 0
 Best Local Similarity: 97.74% Mismatches: 6
 Query Match: 75.05% Indels: 5
 DB: 13 Gaps: 0

US-10-063-670-6 (1-322) x BX402505 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrrpThrArgLeuLeu 20
 DB 212 ATGCCAGGCTTCAGCGCTGGTGTGCTTCCACTCCATCTGACACGAGGCTCTG 271
 QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
 DB 272 GTCCAGGCTTTGGCGTGCAGAGAGCTTTCCATCCAGGTGTGATGAGATTATGGGG 331
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPhetheThrGluAlaLysGluAla 60
 DB 332 ATCACCTTGTGAGCAAAAGCGCAACAGCAGCTGAATTTACAGAAAGCTTAAGGAGGCC 391
 QY 61 CysArgIleuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
 DB 392 TGTAGGCTGTGGGACTAAGTTTGGCCGCGCAAGGACCAAGTTGAACAGCCTTGAAGACT 451
 QY 81 SerPheGluThrCysSerTyrGlyTrrpValGlyAspGlyPheValValIleSerArgIle 100
 DB 452 AGCTTTGAACCTTGACGATATGGCTGGTGGTGGAGATGATTCGTTGATCTCTAGGATT 511
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrpLysValProVal 120
 DB 512 AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTGATTTGGAAGGTTCCAGTG 571
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrpThrAsnSerCysIle 140
 DB 572 AGCCGACAGTTTGGCGCTATTGTTACAACTCATCTGATCTGACCTAACTCGTGCATT 631
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
 DB 632 CCAGAAATTATCACCAACCAAGATCCCATATTCACACTCAAACTGCAACAAACAACA 691
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

692 GAATTTATGTCTAGTGACAGTACCTACTCGGTGGCATCCCTTACTTACAAATACCTGCC 751
 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
 752 CCTACTACT 811
 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
 812 TGTGTCTCAGAGAAGTTTTATGTGAAACTAGCACCATGCTCTACAGAAACTGAACCATTTGTT 871
 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
 872 GAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGTTTGGAGTGT-CCACACGCTCTG 930
 241 LeuValLeuAlaLeuLeuPhePheGlyValAlaAlaGlyLeuGlyPheCysTyrValLys 260
 931 CTAGTGTCTGTCT-CTCTTCTTTGGTGTCTGAGY-GGTCTTGGATTGGS-TAATKTCAAA 987
 261 ArgTyrValLysAla 265
 988 AG-TATGTGAAGGCT 1001

RESULT 15
 AL544430 1201 bp mRNA linear EST 31-MAY-2003
 LOCUS AL544430 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CSODI018YG12 5-PRIME, mRNA sequence.
 ACCESSION AL544430
 VERSION AL544430.2 GI:31266274
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12876910.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5952.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSODI018BD06QPl&cluster=5952.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSODI018BD06QPl.

FEATURES
 source
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODI018YG12"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Alignment Scores:
 Pred. No.: 2.2e-104 Length: 1201
 Score: 1243.00 Matches: 256
 Percent Similarity: 95.90% Conservative: 1
 Best Local Similarity: 95.52% Mismatches: 9
 Query Match: 75.02% Indels: 5
 DB: 9 Gaps: 2

US-10-063-670-6 (1-322) x AL544430 (1-1201)

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QY      1  MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTyrThrThrArgLeuLeu 20
Db      239  ATGGCCAGGTGTTTCAGCGTGGTGTGCTTCTCACTTCATCTGGACCACGAGGCTCCTG 298
QY     21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db     299  GTCCAGGCTCTTTGCGTGCAAGAAGACTTTCATCCAGGTGTCAAGCAGAAATTATGGGG 358
QY     41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db     359  ATCACCCCTTGTGAGCAAAAGCGAACACGACGAGCTGAATTTCCACAGAGCTAAGGAGGCC 418
QY     61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db     419  TGTAGGCTGCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 478
QY     81  SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db     479  AGCTTTGAACCTTGACAGCTATGCGCTGGGTGGAGATGGATTCGTGTCATCTCTAGGATT 538
QY    101  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal 120
Db     539  AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 598
QY    121  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThrAsnSerCysIle 140
Db     599  AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTGGACTTAACCTCGTGCAAT 658
QY    141  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db     659  CCAGAAATATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 718
QY    161  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db     719  GAATTTATTGTCAGTCACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 778
QY    181  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db     779  CCTACTACTACTCCTCCTCCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 838
QY    201  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db     839  TGTGTCACAGAAGTTTATTGGAACCTAGCACCATGCTCTACAGAACTGAACCAATTGTT 898
QY    221  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db     899  GAAATATAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGT-CCCACGGCTCTG 957
QY    241  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db     958  CTAGTGCTTGCTCT-CTCTCTCTTGTGCKGSAGYGGTCT---TGGATTTGCTATGTCAA- 1012
QY    261  ArgTyrValLysAlaPheProPhe 268
Db    1013  AGGTATGTRAGGCYT---CCCTTT 1033
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Search completed: August 17, 2004, 01:23:10
Job time : 3054 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2004, 01:24:53 ; Search time 538 Seconds
(without alignments)
2936.669 Million cell updates/sec

Title: US-10-063-670-6

Perfect score: 1657

Sequence: 1 MARCFSLVLLNLSIWTRLL.....NPEESKSPKTTVRCLEAEV 322

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 800 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US10063670/runat_10082004_165530_14795/app query.fasta_1.519
-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=800 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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1	1657	100.0	2029	15	US-10-079-111-2	Sequence 2, Appli
2	1657	100.0	2372	9	US-09-909-320-200	Sequence 200, App
3	1657	100.0	2372	9	US-09-909-088B-200	Sequence 200, App
4	1657	100.0	2372	9	US-09-905-291A-200	Sequence 200, App
5	1657	100.0	2372	9	US-09-902-853-200	Sequence 200, App
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8	1657	100.0	2372	10	US-09-904-011-200	Sequence 200, App
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135	1657	100.0	2372	15	US-10-063-724-5	Sequence 5, Appli	208	1657	100.0	2372	15	US-10-063-666-5	Sequence 5, Appli
136	1657	100.0	2372	15	US-10-063-727-5	Sequence 5, Appli	209	1657	100.0	2372	15	US-10-063-672-5	Sequence 5, Appli
137	1657	100.0	2372	15	US-10-063-730-5	Sequence 5, Appli	210	1657	100.0	2372	15	US-10-063-682-5	Sequence 5, Appli
138	1657	100.0	2372	15	US-10-063-734-5	Sequence 5, Appli	211	1657	100.0	2372	15	US-10-063-721-5	Sequence 5, Appli
139	1657	100.0	2372	15	US-10-063-736-5	Sequence 5, Appli	212	1657	100.0	2372	15	US-10-063-723-5	Sequence 5, Appli
140	1657	100.0	2372	15	US-10-063-742-5	Sequence 5, Appli	213	1657	100.0	2372	15	US-10-063-514-5	Sequence 5, Appli
141	1657	100.0	2372	15	US-10-063-743-5	Sequence 5, Appli	214	1657	100.0	2372	15	US-10-063-516-5	Sequence 5, Appli
142	1657	100.0	2372	15	US-10-063-744-5	Sequence 5, Appli	215	1657	100.0	2372	15	US-10-063-529-5	Sequence 5, Appli
143	1657	100.0	2372	15	US-10-063-565-5	Sequence 5, Appli	216	1657	100.0	2372	15	US-10-063-937-200	Sequence 200, App
144	1657	100.0	2372	15	US-10-063-577-5	Sequence 5, Appli	217	1657	100.0	2372	15	US-10-063-684-5	Sequence 5, Appli
145	1657	100.0	2372	15	US-10-063-591-5	Sequence 5, Appli	218	1657	100.0	2372	15	US-10-063-688-5	Sequence 5, Appli
												US-10-223-081-31	Sequence 31, Appli

219	1657	100.0	2372	15	US-10-063-520-5	Sequence 5, Appli	292	145	8.8	1414	9	US-09-799-118-1	Sequence 1, Appli
220	1657	100.0	2372	15	US-10-063-647-5	Sequence 5, Appli	293	143.5	8.7	336	10	US-09-918-995-17767	Sequence 17767, A
221	1657	100.0	2372	15	US-10-063-548-5	Sequence 5, Appli	294	143.5	8.7	431	13	US-10-424-599-106015	Sequence 106015,
222	1657	100.0	2372	15	US-10-063-578-5	Sequence 5, Appli	295	142.5	8.6	8444	16	US-10-028-248A-1	Sequence 1, Appli
223	1657	100.0	2372	15	US-10-063-648-5	Sequence 5, Appli	296	142.5	8.6	8444	16	US-10-107-782-1	Sequence 1, Appli
224	1657	100.0	2372	15	US-10-063-677-5	Sequence 5, Appli	297	141.5	8.5	8495	16	US-10-028-248A-3	Sequence 3, Appli
225	1657	100.0	2372	15	US-10-063-718-5	Sequence 5, Appli	298	141.5	8.5	8495	16	US-10-107-782-3	Sequence 3, Appli
226	1657	100.0	2372	15	US-10-063-741-5	Sequence 5, Appli	299	138.5	8.4	1411	9	US-09-765-231A-44	Sequence 44, Appl
227	1657	100.0	2372	15	US-10-063-617-5	Sequence 5, Appli	300	137	8.3	3260	16	US-10-028-248A-210	Sequence 210, App
228	1657	100.0	2372	15	US-10-223-082-31	Sequence 31, Appli	301	137	8.3	3260	16	US-10-107-782-210	Sequence 210, App
229	1657	100.0	2372	15	US-10-063-664-5	Sequence 5, Appli	302	137	8.3	4576	9	US-09-842-930A-24	Sequence 24, App
230	1657	100.0	2372	15	US-10-063-561-5	Sequence 5, Appli	303	137	8.3	4642	15	US-10-133-172-3	Sequence 3, Appli
231	1657	100.0	2372	15	US-10-063-618-5	Sequence 5, Appli	304	137	8.3	4642	15	US-10-133-172-3	Sequence 19, Appl
232	1657	100.0	2372	15	US-10-063-657-5	Sequence 5, Appli	305	136	8.2	4706	9	US-09-842-930A-1	Sequence 1, Appli
233	1657	100.0	2372	15	US-10-063-668-5	Sequence 5, Appli	306	136	8.2	4706	9	US-09-842-930A-1	Sequence 19, Appl
234	1657	100.0	2372	16	US-10-063-550-5	Sequence 5, Appli	307	135.5	8.2	4706	15	US-10-133-172-1	Sequence 1, Appli
235	1657	100.0	2372	16	US-10-449-656-200	Sequence 200, App	308	135.5	8.2	3153	10	US-09-759-130B-343	Sequence 343, App
236	1657	100.0	2372	16	US-10-448-713-200	Sequence 200, App	309	135.5	8.2	3153	15	US-10-189-123-73	Sequence 73, Appl
237	1657	100.0	2372	17	US-10-425-447-200	Sequence 200, App	310	135.5	8.2	3153	15	US-10-188-495-73	Sequence 73, Appl
238	1657	100.0	2372	17	US-10-215-371-200	Sequence 200, App	311	132.5	8.0	2160	16	US-10-741-790-343	Sequence 343, App
239	1657	100.0	2404	9	US-09-833-381-849	Sequence 849, App	312	131.5	7.9	2652	13	US-10-104-047-1824	Sequence 1824, Ap
240	1657	100.0	2404	9	US-09-833-381-853	Sequence 853, App	313	131.5	7.9	2652	15	US-10-453-420-4	Sequence 4, Appli
241	1654	99.8	2324	13	US-10-276-774-999	Sequence 999, App	314	131	7.9	2013	10	US-09-759-130B-330	Sequence 330, App
242	1651	99.6	2313	15	US-10-291-634-1	Sequence 1, Appli	315	131	7.9	2013	15	US-10-189-123-60	Sequence 60, Appl
243	1651	99.6	2369	16	US-10-264-237-1260	Sequence 1260, Ap	316	131	7.9	2013	15	US-10-188-495-60	Sequence 60, Appl
244	1511.5	91.2	1127	16	US-10-138-588-1	Sequence 1, Appli	317	131	7.9	2013	17	US-10-741-790-330	Sequence 330, App
245	1103	66.6	1896	10	US-09-866-050A-595	Sequence 595, App	318	131	7.9	2730	10	US-09-759-130B-329	Sequence 329, App
246	1103	66.6	1896	15	US-10-152-661-595	Sequence 595, App	319	131	7.9	2730	15	US-10-189-123-59	Sequence 59, Appl
247	673	40.6	411	10	US-09-918-995-8107	Sequence 8107, Ap	320	131	7.9	2730	15	US-10-188-495-59	Sequence 59, Appl
248	595.5	35.9	559	15	US-10-079-111-3	Sequence 3, Appli	321	131	7.9	2730	17	US-10-741-790-329	Sequence 329, App
249	440	26.6	486	10	US-10-079-111-4	Sequence 4, Appli	322	131	7.9	3438	13	US-10-312-352-60	Sequence 60, Appl
250	386	23.3	279	15	US-10-091-634-12	Sequence 12, Appli	323	131	7.9	3476	13	US-10-245-752-51	Sequence 51, Appl
251	354	21.4	492	15	US-10-291-634-13	Sequence 13, Appli	324	131	7.9	3476	13	US-10-245-859-51	Sequence 51, Appl
252	349	21.1	466	15	US-09-864-761-2325	Sequence 2325, Ap	325	131	7.9	3476	15	US-10-245-103-51	Sequence 51, Appl
253	306	18.5	469	9	US-09-864-761-19060	Sequence 15, Appl	326	131	7.9	3476	15	US-10-245-107-51	Sequence 51, Appl
254	286.5	17.3	498	15	US-09-864-761-15431	Sequence 15431, A	327	131	7.9	3476	15	US-10-245-143-51	Sequence 51, Appl
255	281.5	17.0	457	9	US-09-917-800A-1588	Sequence 1588, Ap	328	131	7.9	3476	15	US-10-245-71-51	Sequence 51, Appl
256	231	13.9	1747	9	US-10-101-510-436	Sequence 436, App	329	131	7.9	3476	15	US-10-245-851-51	Sequence 51, Appl
257	223	13.5	1992	15	US-09-864-761-19060	Sequence 19060, A	330	131	7.9	3476	15	US-10-237-535-51	Sequence 51, Appl
258	222	13.4	141	9	US-09-864-761-19060	Sequence 31, Appl	331	131	7.9	3476	15	US-10-237-535-51	Sequence 51, Appl
259	215	13.0	1354	12	US-09-836-544-31	Sequence 31, Appl	332	131	7.9	3476	15	US-10-238-183-51	Sequence 51, Appl
260	213	12.9	1794	15	US-10-007-926A-376	Sequence 376, App	333	131	7.9	3476	15	US-10-238-283-51	Sequence 51, Appl
261	212	12.8	1981	15	US-10-084-817-180	Sequence 180, App	334	131	7.9	3476	15	US-10-238-370-51	Sequence 51, Appl
262	212	12.8	4365	15	US-10-247-671-72	Sequence 72, Appl	335	131	7.9	3476	15	US-10-245-055-51	Sequence 51, Appl
263	212	12.8	5165	10	US-09-814-363-20099	Sequence 20099, A	336	131	7.9	3476	15	US-10-245-147-51	Sequence 51, Appl
264	210	12.7	1297	17	US-10-641-643-876	Sequence 876, App	337	131	7.9	3476	15	US-10-245-739-51	Sequence 51, Appl
265	199.5	12.0	2100	15	US-10-042-969C-1	Sequence 1, Appli	338	131	7.9	3476	15	US-10-246-210-51	Sequence 51, Appl
266	199.5	12.0	2308	12	US-09-836-544-33	Sequence 33, Appl	339	131	7.9	3476	15	US-10-239-136-51	Sequence 51, Appl
267	199.5	12.0	2316	10	US-09-983-000A-15	GENERAL INFORMATI	340	131	7.9	3476	15	US-10-239-136-51	Sequence 51, Appl
268	199.5	12.0	4674	9	US-09-974-298-22	Sequence 22, Appl	341	131	7.9	3476	15	US-10-243-024-51	Sequence 51, Appl
269	199.5	12.0	4674	10	US-09-971-429B-51	Sequence 51, Appl	342	131	7.9	3476	15	US-10-243-409-51	Sequence 51, Appl
270	199.5	12.0	4674	15	US-10-084-817-181	Sequence 181, App	343	131	7.9	3476	15	US-10-245-621-51	Sequence 51, Appl
271	197	11.9	2387	17	US-10-648-593-41	Sequence 41, Appl	344	131	7.9	3476	15	US-10-245-880-51	Sequence 51, Appl
272	197	11.9	2905	14	US-10-044-090-495	Sequence 495, App	345	131	7.9	3476	15	US-10-245-033-51	Sequence 51, Appl
273	197	11.9	3474	9	US-09-981-353-9	Sequence 9, Appli	346	131	7.9	3476	15	US-10-243-095-51	Sequence 51, Appl
274	170	10.3	106	9	US-09-864-761-31946	Sequence 31946, A	347	131	7.9	3476	15	US-10-245-185-51	Sequence 51, Appl
275	166.5	10.0	399	10	US-09-918-995-36412	Sequence 36412, A	348	131	7.9	3476	15	US-10-245-427-51	Sequence 51, Appl
276	165	10.0	820	15	US-10-079-111-5	Sequence 5, Appli	349	131	7.9	3476	15	US-10-245-473-51	Sequence 51, Appl
277	158	9.5	549	15	US-10-101-510-85	Sequence 85, Appl	350	131	7.9	3476	15	US-10-245-770-51	Sequence 51, Appl
278	153.5	9.3	270	10	US-09-927-463-7	Sequence 7, Appli	351	131	7.9	3476	15	US-10-245-877-51	Sequence 51, Appl
279	151	9.1	2863	16	US-10-104-047-610	Sequence 610, App	352	131	7.9	3476	15	US-10-246-976-51	Sequence 51, Appl
280	148.5	9.0	425	10	US-09-918-995-35733	Sequence 44, App	353	131	7.9	3476	15	US-10-243-320-51	Sequence 51, Appl
281	148.5	9.0	836	13	US-10-027-632-148987	Sequence 124, App	354	131	7.9	3476	15	US-10-242-743-51	Sequence 51, Appl
282	148.5	9.0	836	16	US-10-027-632-148987	Sequence 291, App	355	131	7.9	3476	15	US-10-242-845-51	Sequence 51, Appl
283	145.5	8.8	1144	14	US-10-044-090-446	Sequence 148987, A	356	131	7.9	3476	15	US-10-237-636-51	Sequence 51, Appl
284	145.5	8.8	1144	15	US-10-247-671-124	Sequence 446, App	357	131	7.9	3476	15	US-10-238-325-51	Sequence 51, Appl
285	145.5	8.8	1422	16	US-10-295-027-291	Sequence 291, App	358	131	7.9	3476	15	US-10-238-325-51	Sequence 51, Appl
286	145.5	8.8	1430	16	US-10-295-027-1020	Sequence 1020, Ap	359	131	7.9	3476	15	US-10-238-461-51	Sequence 51, Appl
287	145.5	8.8	1728	14	US-10-044-090-445	Sequence 445, App	360	131	7.9	3476	15	US-10-243-124-51	Sequence 51, Appl
288	145.5	8.8	7840	12	US-10-634-574-15	Sequence 15, Appl	361	131	7.9	3476	15	US-10-243-425-51	Sequence 51, Appl
289	145	8.8	351	15	US-10-060-036-880	Sequence 880, App	362	131	7.9	3476	15	US-10-243-446-51	Sequence 51, Appl
290	145	8.8	466	13	US-10-085-783A-58386	Sequence 58386, A	363	131	7.9	3476	15	US-10-245-874-51	Sequence 51, Appl
291	145	8.8	466	16	US-10-242-535A-58386	Sequence 58386, A	364	131	7.9	3476	15	US-10-242-653-51	Sequence 51, Appl

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366	131	7.9	3476	15	US-10-243-388-51	Sequence 51, Appl	439	127.5	7.7	1985	9	US-09-902-853-212	Sequence 212, App
367	131	7.9	3476	15	US-10-244-947-51	Sequence 51, Appl	440	127.5	7.7	1985	9	US-09-907-824-212	Sequence 212, App
368	131	7.9	3476	15	US-10-244-968-51	Sequence 51, Appl	441	127.5	7.7	1985	9	US-09-907-841-212	Sequence 212, App
369	131	7.9	3476	15	US-10-244-990-51	Sequence 51, Appl	442	127.5	7.7	1985	10	US-09-904-011-212	Sequence 212, App
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371	131	7.9	3476	15	US-10-245-127-51	Sequence 51, Appl	444	127.5	7.7	1985	10	US-09-906-838-212	Sequence 212, App
372	131	7.9	3476	15	US-10-245-207-51	Sequence 51, Appl	445	127.5	7.7	1985	10	US-09-907-613-212	Sequence 212, App
373	131	7.9	3476	15	US-10-245-646-51	Sequence 51, Appl	446	127.5	7.7	1985	10	US-09-904-859-212	Sequence 212, App
374	131	7.9	3476	15	US-10-245-695-51	Sequence 51, Appl	447	127.5	7.7	1985	10	US-09-909-204-212	Sequence 212, App
375	131	7.9	3476	15	US-10-245-699-51	Sequence 51, Appl	448	127.5	7.7	1985	10	US-09-904-820-212	Sequence 212, App
376	131	7.9	3476	15	US-10-245-737-51	Sequence 51, Appl	449	127.5	7.7	1985	10	US-09-904-786-212	Sequence 212, App
377	131	7.9	3476	15	US-10-245-878-51	Sequence 51, Appl	450	127.5	7.7	1985	10	US-09-906-646-212	Sequence 212, App
378	131	7.9	3476	15	US-10-245-890-51	Sequence 51, Appl	451	127.5	7.7	1985	10	US-09-906-700-212	Sequence 212, App
379	131	7.9	3476	15	US-10-245-899-51	Sequence 51, Appl	452	127.5	7.7	1985	10	US-09-903-786-212	Sequence 212, App
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381	131	7.9	3476	15	US-10-247-058-51	Sequence 51, Appl	454	127.5	7.7	1985	10	US-09-904-119-212	Sequence 212, App
382	131	7.9	3476	15	US-10-245-454-51	Sequence 51, Appl	455	127.5	7.7	1985	10	US-09-904-956-212	Sequence 212, App
383	131	7.9	3476	15	US-10-237-471-51	Sequence 51, Appl	456	127.5	7.7	1985	10	US-09-902-736-212	Sequence 212, App
384	131	7.9	3476	15	US-10-238-261-51	Sequence 51, Appl	457	127.5	7.7	1985	10	US-09-907-794-212	Sequence 212, App
385	131	7.9	3476	15	US-10-238-324-51	Sequence 51, Appl	458	127.5	7.7	1985	10	US-09-903-943-212	Sequence 212, App
386	131	7.9	3476	15	US-10-241-860-51	Sequence 51, Appl	459	127.5	7.7	1985	10	US-09-904-462-212	Sequence 212, App
387	131	7.9	3476	15	US-10-242-172-51	Sequence 51, Appl	460	127.5	7.7	1985	10	US-09-907-925-212	Sequence 212, App
388	131	7.9	3476	15	US-10-242-652-51	Sequence 51, Appl	461	127.5	7.7	1985	10	US-09-902-692-212	Sequence 212, App
389	131	7.9	3476	15	US-10-242-990-51	Sequence 51, Appl	462	127.5	7.7	1985	10	US-09-903-520-212	Sequence 212, App
390	131	7.9	3476	15	US-10-243-023-51	Sequence 51, Appl	463	127.5	7.7	1985	10	US-09-905-056-212	Sequence 212, App
391	131	7.9	3476	15	US-10-243-103-51	Sequence 51, Appl	464	127.5	7.7	1985	10	US-09-907-794-212	Sequence 212, App
392	131	7.9	3476	15	US-10-243-276-51	Sequence 51, Appl	465	127.5	7.7	1985	10	US-09-903-943-212	Sequence 212, App
393	131	7.9	3476	15	US-10-243-326-51	Sequence 51, Appl	466	127.5	7.7	1985	10	US-09-904-462-212	Sequence 212, App
394	131	7.9	3476	15	US-10-243-364-51	Sequence 51, Appl	467	127.5	7.7	1985	10	US-09-905-381-212	Sequence 212, App
395	131	7.9	3476	15	US-10-243-494-51	Sequence 51, Appl	468	127.5	7.7	1985	10	US-09-905-088-212	Sequence 212, App
396	131	7.9	3476	15	US-10-244-995-51	Sequence 51, Appl	469	127.5	7.7	1985	10	US-09-907-575-212	Sequence 212, App
397	131	7.9	3476	15	US-10-245-230-51	Sequence 51, Appl	470	127.5	7.7	1985	10	US-09-905-075-212	Sequence 212, App
398	131	7.9	3476	15	US-10-245-253-51	Sequence 51, Appl	471	127.5	7.7	1985	10	US-09-902-759-212	Sequence 212, App
399	131	7.9	3476	15	US-10-245-479-51	Sequence 51, Appl	472	127.5	7.7	1985	10	US-09-902-634-212	Sequence 212, App
400	131	7.9	3476	15	US-10-245-499-51	Sequence 51, Appl	473	127.5	7.7	1985	10	US-09-902-713-212	Sequence 212, App
401	131	7.9	3476	15	US-10-245-772-51	Sequence 51, Appl	474	127.5	7.7	1985	10	US-09-902-979-212	Sequence 212, App
402	131	7.9	3476	15	US-10-245-811-51	Sequence 51, Appl	475	127.5	7.7	1985	10	US-09-902-615-212	Sequence 212, App
403	131	7.9	3476	15	US-10-245-812-51	Sequence 51, Appl	476	127.5	7.7	1985	10	US-09-903-925-212	Sequence 212, App
404	131	7.9	3476	15	US-10-245-852-51	Sequence 51, Appl	477	127.5	7.7	1985	10	US-09-906-760A-212	Sequence 212, App
405	131	7.9	3476	15	US-10-245-875-51	Sequence 51, Appl	478	127.5	7.7	1985	10	US-09-903-823-212	Sequence 212, App
406	131	7.9	3476	15	US-10-245-881-51	Sequence 51, Appl	479	127.5	7.7	1985	10	US-09-907-852-212	Sequence 212, App
407	131	7.9	3476	15	US-10-245-911-51	Sequence 51, Appl	480	127.5	7.7	1985	10	US-09-902-572A-212	Sequence 212, App
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412	131	7.9	3476	15	US-10-246-929-51	Sequence 51, Appl	485	127.5	7.7	1985	10	US-09-904-992-212	Sequence 212, App
413	131	7.9	3476	15	US-10-247-036-51	Sequence 51, Appl	486	127.5	7.7	1985	10	US-09-904-838-212	Sequence 212, App
414	131	7.9	3476	15	US-10-243-255-51	Sequence 51, Appl	487	127.5	7.7	1985	10	US-09-906-777-212	Sequence 212, App
415	131	7.9	3476	15	US-10-245-810-51	Sequence 51, Appl	488	127.5	7.7	1985	10	US-09-903-603A-212	Sequence 212, App
416	131	7.9	3476	15	US-10-245-910-51	Sequence 51, Appl	489	127.5	7.7	1985	10	US-09-904-532-212	Sequence 212, App
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697	127.5	7.7	1985	15	US-10-188-774-27	Sequence 27, Appl	770	127.5	7.7	1985	15	US-10-187-752-27	Sequence 27, Appl
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723	127.5	7.7	1985	15	US-10-188-780-27	Sequence 27, Appl	796	127.5	7.7	1985	15	US-10-205-907-27	Sequence 27, Appl
724	127.5	7.7	1985	15	US-10-192-015-27	Sequence 27, Appl	797	127.5	7.7	1985	15	US-10-194-456-27	Sequence 27, Appl
725	127.5	7.7	1985	15	US-10-194-394-27	Sequence 27, Appl	798	127.5	7.7	1985	15	US-10-196-758-27	Sequence 27, Appl
726	127.5	7.7	1985	15	US-10-194-425-27	Sequence 27, Appl	799	127.5	7.7	1985	15	US-10-198-770-27	Sequence 27, Appl
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GenCore version 5.1.6
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Run on: August 16, 2004, 23:31:04 ; Search time 91 Seconds
(without alignments)
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Title: US-10-063-670-6

Perfect score: 1657

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Fgapop 6.0 , Fgapext 7.0
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1657	100.0	2372	4	US-09-902-775A-200
5	1657	100.0	2404	4	US-09-833-381-849
6	1657	100.0	2404	4	US-09-833-381-853
7	1651	99.6	2313	2	US-08-892-880-1
8	1103	66.6	1896	4	US-09-724-864-28
9	354	21.4	492	2	US-08-892-880-12
10	349	21.1	466	2	US-08-892-880-13
11	286.5	17.3	498	2	US-08-892-880-15
12	234.5	14.2	1537	6	5504194-1

13	224	13.5	3207	1	US-07-946-497-1	Sequence 1, Appli
14	224	13.5	3207	1	US-08-483-322-1	Sequence 1, Appli
15	224	13.5	3207	2	US-08-478-882-1	Sequence 1, Appli
16	213	12.9	1794	3	US-09-213-719-1	Sequence 1, Appli
17	210	12.7	1297	4	US-09-023-655-876	Sequence 876, App
18	199.5	12.0	4675	4	US-09-566-921-97	Sequence 97, Appl
19	145	8.8	1414	1	US-08-024-868-1	Sequence 1, Appli
20	145	8.8	1414	2	US-08-242-097-1	Sequence 1, Appli
21	145	8.8	1414	3	US-09-206-695-1	Sequence 1, Appli
22	145	8.8	1414	4	US-09-799-118-1	Sequence 1, Appli
23	133.5	8.1	1734	4	US-09-484-970B-63	Sequence 63, Appl
24	128.5	7.8	3259	5	PCT-US95-03747-1	Sequence 1, Appli
25	127.5	7.7	1985	4	US-09-907-794A-212	Sequence 212, App
26	127.5	7.7	1985	4	US-09-905-125A-212	Sequence 212, App
27	127.5	7.7	1985	4	US-09-902-775A-212	Sequence 212, App
28	121	7.3	1587	4	US-09-010-147B-19	Sequence 19, Appl
29	114.5	6.9	5191	1	US-08-340-428B-1	Sequence 1, Appli
30	114.5	6.9	5191	5	PCT-US93-07306-1	Sequence 1, Appli
31	113	6.8	8224	6	5180808-1	Patent No. 5180808
32	112	6.8	1190	1	US-08-310-370-1	Sequence 1, Appli
33	111	6.7	1720	4	US-09-148-545-53	Sequence 53, Appl
34	107	6.5	1400	2	US-08-001-078A-2	Sequence 2, Appli
35	107	6.5	1400	2	US-08-463-218-2	Sequence 2, Appli
36	107	6.5	1400	5	PCT-US94-00253-2	Sequence 2, Appli
37	107	6.5	1520	1	US-08-225-477B-1	Sequence 1, Appli
38	107	6.5	1520	5	PCT-US95-04353-1	Sequence 1, Appli
39	107	6.5	2589	1	US-08-325-267A-3	Sequence 3, Appli
40	107	6.5	2685	3	US-08-362-525-21	Sequence 21, Appl
41	107	6.5	4614	1	US-08-325-267A-1	Sequence 1, Appli
42	106.5	6.4	1482	4	US-09-016-434-230	Sequence 230, App
43	106.5	6.4	2455	3	US-09-103-429A-1	Sequence 1, Appli
44	106.5	6.4	2821	3	US-09-103-429A-2	Sequence 2, Appli
45	103	6.2	1519	1	US-08-225-477B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-232-160-13
; Sequence 13, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:

; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232,160
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 13

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 3044710
US-09-232-160-13

Alignment Scores:
Pred. No.: 4.6e-177 Length: 2029
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

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Qy 21 ValGlnGlySerLeuArgAlaGluGluSerLeuValSerCysArgIleMetGly 40
Db 243 GTCCAGGCTCTTTGGCTGCAGAGAGCTTTCCATCCAGGTGTCTCAGAAATATATGGG 302
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 303 ATACCCCTTTGTGACAAAGGCCAACCCAGCAGCTGAATTCACAGAGCTTAAGAGGCC 362
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal 120
Db 483 AGCCCAACCCCAAGTGTGGGAAAATGGGTGGGTGCTGCTGATTGGAGGTTCCAGTG 542
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrThrThrAsnSerCysIle 140
Db 543 AGCCGACAGTTTGCAGCTATTTGTACAACTCATCTGATCTGACTTAACCTCGTCATT 602
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 603 CCAGAAATTAATACCCACCAAGATGCCATATTCACCACTCAAACTGCAACCAACAACA 662
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 663 GAATTTATTTGTCAGTGACAGTACCTACTCGTGGCATCCCTTACTTACTCAATACCTGCC 722
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysIle 200
Db 723 CCTACTACTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 782
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 783 TGTGTACAGAAAGTTTATGGAACTAGCACCATGCTCAGAACTGAAACCTATTTGTT 842
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 843 GAAATAAAGCAGCATTCAGAAATGAAGTCTGGTGGGTGAGGTGCTCCACAGCTCTG 902
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 903 CTAGTGTCTGCTCAA 962
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 963 AGGTATGTGAAGGCTTCCCTTTTACAAACAGAAATCAGCAGAGAAATGATCGAAACC 1022
Qy 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1023 AAAGTAGTAAGAGGAGAGAGGCCAAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1082
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1083 GATAAAACCCAGAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGCT 1142
Qy 321 GluVal 322
Db 1143 GAAGTT 1148

RESULT 2

US-09-907-794A-200
; Sequence 200, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
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; PRIOR FILING DATE: 1999-12-20
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; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
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; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-794A-200

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Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0

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Query Match:	100.00%	Indels:	0
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QY	21	ValGlnGlySerLeuArgAlaGlnGluLeuSerIleGlnValSerCysArgIleMetGly	40
DB	220	GTCCAAAGGCTCTTGGCTGCAAGAGCTTCCATCCAGGTGTCAAGCAAGTATGCGG	279
QY	41	IleThrLeuValSerIlyslsAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
DB	280	ATCACCCCTGTGAGCAAAAGCGCAACACAGCAGCTGAATTTCCACAGAAGCTAAGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
DB	340	TGTAGGCTGTGGGACTAAGTTTGGCGGACAGGACCAAGTTGAACAGCCCTTGAAGCT	399
QY	81	SerpheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle	100
DB	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGCTCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrIlyslsValProVal	120
DB	460	AGCCCAAAACCCCAAGTGGGAAATGGGGTGGTCTGATTTGGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThrAsnSerCysIle	140
DB	520	AGCCACAGCTTGCAGCTATTTGTACACTCATCTGACTTGAACCTGTCGTCATT	579
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DB	760	TGTGTACAGAAAGTTTATGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheIlyslsAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
DB	820	GAAATAAAGCAGCATTCAGAAATGAAGTGTCTGGGTGTGGAGGTGTCCCAACGGCTCTG	879
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DB	880	CTAGTGTCTGCTCTCTCTCTTCTGCTGCTGAGCTGTGCTTGGATTTGCTATGTCAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
DB	940	AGGTATGTGAAGGCTTCCCTTTTCAAAACAAGAAATCAGCAGAGAAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerIlyslsThr	300
DB	1000	AAAGTAGTAAGAGGAGAGGCCAATGATACCAACCCCTTAATGAGGAATCAAGAAAACT	1059
QY	301	AspLysAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
DB	1060	GATAAAACCCCAAGAGTCCCAAGAGTCCCAAGAACTTACCCTGCGATGCGCTGGAAGCT	1119
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RESULT 3
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; Sequence 200, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372


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/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 200
/ LENGTH: 2372
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-902-775A-200

Alignment Scores:
Pred. No.: 5,92e-177 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-063-670-6 (1-322) x US-09-902-775A-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTACAGCTGGTGTCTTCTCACTTCCATCTGGACACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAGAGGCTCTTTGGTGCAGAGAGCTTTCATCCAGGTGTCAATGAGAAATATATGGGG 279
QY 41 IleThrLeuValSerIlySerIlyAlaAsnGlnGlnLeuAsnPheThrGluAlaIlyGluAla 60
Db 280 ATCAACCTTGTGAGCAAAAGGACCAACGACGCTGAATTTACAGAACTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyIlyAspGlnValGluThrAlaLeuIlyAla 80
Db 340 TGTAGCTCTCGGACTAAGTTTGGCGGCAAGCAAGTTCAAACAGCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleValIleSerArgIle 100
Db 400 AGCTTTGAAACTTTCAGCTATGCTGGTGGTGGAGATGGATTCGTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyIlyAsnGlyValGlyValLeuIleTrpIlyValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGGAAATGGGTGGTGTCTCTGATTTGGAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTGTTCAGCTATTTGTACAACTCATCTGATPACTTGGACTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrIlyAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATATACCCACCAAGATCCCATTTCAACACTCAAACTGCAACACAAACAA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATGTTCAGTGACAGTACTACTCGTGGATCCCTTACTCTACATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgIlyIlyLeuLeu 200
Db 700 CCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAGATTTTATGAAACTATGACCATGTCTACAGAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAATATAAGCAGCATTCAAGATAGAGCTGTCTGGTGTGGAGGTGTCCCCACGCTCTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
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QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGATCAGCAGAGGAAATGATCGAAAC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGlnGluSerLysLysThr 300
Db 1000 AAAGTAGTAGGAGAGGAGGAGCCATATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAGCAAACTACCGTGGATGCTTGGAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 5
US-09-833-381-849
/ Sequence 849, Application US/09833381
/ Patent No. 6672186
/ GENERAL INFORMATION:
/ APPLICANT: Robison, Keith E.
/ TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
/ FILE REFERENCE: 5800-119
/ CURRENT APPLICATION NUMBER: US/09/833,381
/ CURRENT FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: 09/516,448
/ PRIOR FILING DATE: 2000-02-29
/ NUMBER OF SEQ ID NOS: 2050
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 849
/ LENGTH: 2404
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-833-381-849
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Alignment Scores:
Pred. No.: 6,05e-177 Length: 2404
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-063-670-6 (1-322) x US-09-833-381-849 (1-2404)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 190 ATGGCCAGGTGCTTACAGCTGGTGTCTTCTCACTTCCATCTGGACACGAGGCTCCTG 249
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 250 GTCCAGAGGCTCTTTGGTGCAGAGAGCTTTCATCCAGGTGTCAATGAGAAATATATGGGG 309
QY 41 IleThrLeuValSerIlySerIlyAlaAsnGlnGlnLeuAsnPheThrGluAlaIlyGluAla 60
Db 310 ATCAACCTTGTGAGCAAAAGGACCAACGAGCTGGAATTTACAGAACTAAGGAGGCC 369
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuIlyAla 80
Db 370 TGTAGCTCTCGGACTAAGTTTGGCCGCGAGGACCAAGTTGAACAGCTTGAAGCT 429
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 430 AGCTTTGAAACTTTCAGCTATGCTGGTGGTGGAGATGGATTCGTGTCATCTCTAGGATT 489
QY 101 SerProAsnProLysCysGlyIlyAsnGlyValGlyValLeuIleTrpIlyValProVal 120
Db 490 AGCCCAACCCCAAGTGTGGGAAATGGGTGGTGTCTCTGATTTGGAGAGGTTCCAGTG 549
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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Db 550 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCAAT 609
QY 141 ProGluIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 610 CCAGAAATATTATCAACCAAGATGCCATATTCAACTCAACTGCAACCAACAACA 669
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 670 GAATTTTATGTCAGTGACAGTACTCTCGGTGGCATCCCTTACTCTACAAATACCTGCC 729
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 730 CCTACTACTACT 789
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 790 TGTGTACAGAAAGTTTATTGGAACCTAGCACCATGCTCTACAGAAATGAACTTTGTT 849
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 850 GAAATTAAGCAGCATTCAGAAATGAAGCTGCTGGTGGAGGTGTCCTCCACGGCTCTG 909
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 910 CTAGTGCTGCT 969
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 970 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACC 1029
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1030 AAAGTAGTAAGGAGGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1089
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1090 GATAAAAAACCAGAAAGAGTCCAGAGTCCAAAGCAAAACTACCGTGCATGCTCGAAAGCT 1149
QY 321 GluVal 322
Db 1150 GAAGTT 1155

RESULT 6

US-09-833-381-853
; Sequence 853, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 853
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-853

Alignment Scores:
Pred. No.: 6.05e-177 Length: 2404
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-063-670-6 (1-322) x US-09-833-381-853 (1-2404)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleThrThrArgLeuLeu 20

Db 190 ATGGCCAGAGTGTCTTACGCTGGTGTGTTCTTCTCACTTCCATCTGGACCAAGAGCTCCTG 249
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 250 GTCACAGGCTCTTTGGGTGCAGAAAGCTTTTCCATCCAGGTGTCTATCAGAAATATATGGG 309
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 310 ATACACCTTGTGACCAAAAAGGCAACACAGCAGCTGAATTTACAGAAGCTAAGAGGCC 369
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 370 TGTAGGCTGTGGGACTTAAGTTTGGCCGCAAGACCAAGTGAACAGAGCTTGAAGACT 429
QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db 430 AGCTTTGAAACTTGCAGCTATGCTGGGTGGAGATGGATTCGGGTGTCATCTCTAGGATT 489
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 490 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGTCTCTGATTTCGAAAGTTCCAGTG 549
QY 121 SerArgGlnPheAlaLafyrCysTyrAsnSerSerAspThrThrThrAsnSerCysIle 140
Db 550 AGCCGACAGTTTGCAGCCTATTGTTTCAACTCATCTCTGATCTTGGACTTAATCTGTGCAAT 609
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 610 CCAGAAATATTATCAACCAAGATCCCATATTCAACTCAACTCAACTCAACTCAACTCAACT 669
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 670 GAATTTTATGTCAGTGACAGTACTCTCGGTGGCATCCCTTACTCTACAATACCTGCC 729
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 730 CCTACTACTACT 789
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 790 TGTGTACAGAAAGTTTATTGGAACCTAGCACCATGCTCTACAGAAATGAACTTTGTT 849
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 850 GAAATTAAGCAGCATTCAGAAATGAAGCTGCTGGTGGAGGTGTCCTCCACGGCTCTG 909
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 910 CTAGTGCTGCT 969
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 970 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACC 1029
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1030 AAAGTAGTAAGGAGGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1089
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1090 GATAAAAAACCAGAAAGAGTCCAGAGTCCAAAGCAAAACTACCGTGCATGCTCGAAAGCT 1149
QY 321 GluVal 322
Db 1150 GAAGTT 1155

RESULT 7

US-08-892-880-1
; Sequence 1, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN

APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA

ZIP: 20005-3934
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0490001
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2313 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS
LOCATION: 91..1056

FEATURE:

NAME/KEY: mat_peptide
LOCATION: 154..1056

FEATURE:

NAME/KEY: sig_peptide
LOCATION: 91..153

US-08-892-880-1

Alignment Scores:

Pred. No.: 2,71e-176 Length: 2313
Score: 1651.00 Matches: 321

Percent Similarity: 99.69% Conservative: 0
Best Local Similarity: 99.69% Mismatches: 1

Query Match: 99.64% Indels: 0
DB: 2 Gaps: 0

US-10-063-670-6 (1-322) x US-08-892-880-1 (1-2313)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrThrSerIleTrpThrArgLeuLeu 20

Db 91 ATGGCCAGGTGCTTCAGCGTGGTGTCTTCTCACTTCATCTGACACAGGCTCCTG 150

QY 21 ValGlnGlySerLeuArgAlaGluGluSerIleGlnValSerCysArgIleMetGly 40

Db 151 GTCCAGGCTCTTTGGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 210

QY 41 IleThrLeuValSerIleValSerAlaAsnGlnGlnLeuAsnPheThrGluAlaValGluAla 60

Db 211 ATCACCTTGTGAGCAAAAGCGACACAGAGCTGAATTTCCACAGAGCTTAAGAGGCC 270

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyIleValGluThrAlaLeuIleValAla 80

Db 271 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACAGGCTTGAAGCT 330

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 331 AGCTTTGCAACTTGCAGCTATGCTGGGTGGCGATGGATTCGTGCTCATCTCTAGGAT 390
QY 101 SerProAsnProLysCysGlyIleValGlyValLeuIleTrpLysValProVal 120
Db 391 AGCCCAACCCCAAGTGTGGGAAATGGGGTGGTCTCTGATTTGGAGGTTCCAGTG 450
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 451 AGCCGACAGCTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTCAAT 510
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThr 160
Db 511 CCAGAAATTTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 570
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 571 GAATTTATGTCAGTGACAGTACTTCTCGTGGCATCCCTTACTCTACATACCTGCC 630
QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 631 CCTACTACT 690
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 691 TGTGTCACAGAAAGTTTATGGAACACTAGCACCATGTCTACAGAACTGAACCATTTGT 750
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 751 GAAATTAAGCAGCATTTCAAGATGAAGCTGTGGTTTGGAGGTGTCCTCCACGGCTCTG 810
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 811 CTAGTGTCT 870
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 871 AGGTATGTGAAGGCTTCCCTTTTACAAACAGAAATCAGCAGAGAAATGATCGAAACC 930
QY 281 LysValValLysGluLysAlaAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 931 AAAGTAGTAAGGAGGAGAGGCCCAATGATACCAACCTTAATGAGAAATCAAGAAACT 990
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
Db 991 GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGAGTCCAAAGAGTCCAAAGAGTCCAAAG 1050
QY 321 GluVal 322
Db 1051 GAAGTT 1056

RESULT 8

US-09-724-864-28
Sequence 28, Application US/09724864

Patent No. 6380362
GENERAL INFORMATION:

APPLICANT: Watson, James D.
APPLICANT: Murlison, James G.

TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.

FILE REFERENCE: 11000.105001
CURRENT APPLICATION NUMBER: US/09/724,864

PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678

PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28

LENGTH: 1896
TYPE: DNA

ORGANISM: Mouse

US-09-724-864-28		US-09-724-864-28 (1-1896)		US-10-063-670-6 (1-322) x US-08-892-880-12 (1-492)			
Alignment Scores:		Alignment Scores:		Alignment Scores:			
Pred. No.:	1.62e-114	Length:	1896	Pred. No.:	7.76e-31		
Score:	1103.00	Matches:	221	Score:	354.00		
Percent Similarity:	79.18%	Conservative:	30	Percent Similarity:	77.39%		
Best Local Similarity:	69.72%	Mismatches:	62	Best Local Similarity:	72.17%		
Query Match:	66.57%	Indels:	4	Query Match:	21.36%		
DB:	4	Gaps:	3	DB:	2		
US-09-724-864-28 (1-1896)		US-09-724-864-28 (1-1896)		US-10-063-670-6 (1-322) x US-08-892-880-12 (1-492)			
Qy	6	SerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeuValGlnGlySerLeu	25	Qy	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	77	AGCCTGGTGTACTCTCGCTCTATTGGACCACTAGGCACCCAGCTGCAAGTGGCGAC	136	Db	99	ATGCCACGGTCTTTGGTGTGCAGAGAGCTTCCATCCAGGTGTATGCAGAAATATGGG	158
Qy	26	ArgAlaGluLeuSerIleGlnValSerCysArgIleMetGlyIleThrLeuValSer	45	Qy	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	137	CTGCTGCAAGACCTTTCATTTCT--ACATGCAGATCATGGCGGTGGCCTTGTGGGC	193	Db	159	GTCCAGGCTCTTTGGTGTGCAGAGAGCTTCCATCCAGGTGTATGCAGAAATATGGG	218
Qy	46	LysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAlaCysArgLeuLeuGly	65	Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	194	AGAAACAAACCCACAGATGAATTCACAGAACCCACGAGCCTGTAGATGCTGGGA	253	Db	219	ATCACCTTTGTGAGCAAAAGGCAACACAGCAGCTGAAATTTCCAGAAAGCTAAGAGGCC	278
Qy	66	LeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAlaSerPheGluThrCys	85	Qy	61	CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	254	CTGACTCTGGCCAGCAGGACAGGTAGAGTCAGCGCAGAAATCTGGCTTTGAGACTGC	313	Db	279	TGTAGGTGTCTNGGACTAAGTTTGTGGCCGGCAAGCCAGTTG--AAACAGCTTGAAAGT--	334
Qy	86	SerTyrGlyTrpValGlyAspGlyPheValIleSerArgIleSerProAsnProLys	105				
Db	314	AGCTATGGATGGTGGAGAACAGTCTCTGTCTATCCTCGGATTTTCTCAAAACCCGAG	373				
Qy	106	CysGlyLysAsnGlyValGlyValLeuIleTrpLysValProValSerArgGlnPheAla	125				
Db	374	TGTGGGAAGATGCAAGGTGTCTGATTGGAAATGCTCCCTCCAGCCAAAGTTCAAA	433				
Qy	126	AlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIleProGluIleThr	145				
Db	434	GCCTATTGCCACAACCTCATCGACACCTGGGTAACTCTGTCATTCAGAAATCGTTACC	493				
Qy	146	ThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThrGluPheIleValSer	165				
Db	494	ACATTTTACCCCGTGTGGACACTCAA-----ACACCCGCAACAGAGTTTCTGTGTCAGC	547				
Qy	166	AspSerThrTyrSerValAlaSerProTyrSerThrIleProAlaProThrThrPro	185				
Db	548	AGCAGCGCTACTTGGCTTCTATCCCTGACTCCCAACACCTGTCTTCGCCACACCC---	604				
Qy	186	ProAlaProAlaSerThrSerIleProArgArgLysLysLeuIleCysValThrGluVal	205				
Db	605	CGGCTCCACCTTTGACCTCCATGGCAGGAGACAAAAAGATTGTATCACGGAAGTT	664				
Qy	206	PheMetGluThrSerThrMetSerThrGluThrGluProPheValGluAsnLysAlaAla	225				
Db	665	TATACAGAACCTATCACCATGGCTGTACAGAAACAGAACGATTTGTGCAAGTGGAGCAGCA	724				
Qy	226	PheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeuLeuValLeuAlaLeu	245				
Db	725	TTCAGAACAGAGCAGCTGGTGTGGAGGTGTCCACCGCCCTGGTGGCTGCTGCTC	784				
Qy	246	LeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLysArgTyrValLysAla	265				
Db	785	CTCTTCTTGTGTGCTGCGCTGTCTGCTGTCTGCTGTCTGCTGTCTGCTGTCTGCTG	844				
Qy	266	PheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThrLysValValLysGlu	285				
Db	845	TTCCCTTTTCAACCAACCAAGAAATCAACAGAGGAAATGATCGAAACCAAGGTTGTAAGGAA	904				
Qy	286	GluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThrAspLysAsnProGlu	305				
Db	905	GAGAAAGGCTGATGCTCAAGCTATATGAAGATCAAGAAACCAATTAATAAAACCCAGAG	964				
Qy	306	GluSerLysSerProSerLysThrThrValArgCysLeuGluAlaGluVal	322				

Db	965	GAGGCCAAGAGTCCACCCAACTACGGTGGATGCTTAGAGCTGAAGTT	1015
RESULT 9			
US-08-892-880-12			
; Sequence 12, Application US/08892880			
; Patent No. 5942417			
; GENERAL INFORMATION:			
; APPLICANT: NI, JIAN			
; APPLICANT: GENTZ, REINER L.			
; APPLICANT: DILLON, PATRICK J.			
; TITLE OF INVENTION: CD44-LIKE PROTEIN			
; NUMBER OF SEQUENCES: 15			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.			
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600			
; CITY: WASHINGTON			
; STATE: DC			
; COUNTRY: USA			
; ZIP: 20005-3934			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/892,880			
; FILING DATE: HEREWITH			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 60/021,762			
; FILING DATE: 15-JUL-1996			
; ATTORNEY/AGENT INFORMATION:			
; NAME: STEFFE, ERIC K			
; REGISTRATION NUMBER: 36,688			
; REFERENCE/DOCKET NUMBER: 1488.0490001			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 202-371-2600			
; TELEFAX: 202-371-2540			
; INFORMATION FOR SEQ ID NO: 12:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 492 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: cDNA			
US-08-892-880-12			
Alignment Scores:			
Pred. No.:	7.76e-31	Length:	492
Score:	354.00	Matches:	83
Percent Similarity:	77.39%	Conservative:	6
Best Local Similarity:	72.17%	Mismatches:	12
Query Match:	21.36%	Indels:	16
DB:	2	Gaps:	2
US-10-063-670-6 (1-322) x US-08-892-880-12 (1-492)			
Qy	1	MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	99	ATGCCCAAGGTCCTTCAGCTGGTGTCTTTCCTTCCATCTGGACCCAGGCTCTCTG	158
Qy	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	159	GTCCCAAGGCTCTTTCGCTGCAGAAAGAGCTTTCCTCCAGGTGTCTGCAGAAATTATGGG	218
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	219	ATCACCTTGTGTGACAAAAAGCGACAGCTGAATTTTCACAGAACTTAAGAGGCC	278
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	279	TGTAGGTGCTNGACTAAGTTTGGCCGGCAGGCCAGTTG---AACAGCTTGAAGT-	334

QY 81 SerPheGluThrCysSerTyrGlyTTPValGly----- 91
Db 335 AGCTTTGAAT-TGCAGTTTGGCTGGTTGGATGTTCCGNGNCATTTAGTTAGCCCAA 393
QY 92 -----AspGlyPheValValIleSerArgIleSerPro 102
Db 394 OCCANTTTGAAANTGGGTGGNCCNATTTGNAGTCCCTTAGCCCN 438
RESULT 10
US-08-892-880-13
; Sequence 13, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-892-880-13
Alignment Scores:
Pred. No.: 2, 61e-30 Length: 466
Score: 349.00 Matches: 89
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 82.41% Mismatches: 10
Query Match: 21.06% Indels: 8
DB: 2 Gaps: 2
US-10-063-670-6 (1-322) x US-08-892-880-13 (1-466)
QY 219 PheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThr 238
Db 15 TTTGTTGAAATAAAGCAGCATTCAGGAATGAAGCTGCTGGTGGTGGAGGTGTCCTCCACG 74
QY 239 AlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyr 258
Db 75 GCTCTGCTAGTGCCTGCTAT 134
QY 259 ValLysArgTyrVal-LysAlaPheProPheThrAsnLysAsnGlnGlnLys-GluMetI 278

Db 135 GTCAAAAGGTATGTGAAGGCTTCCTTTTCAACAAGATCNCAGAGGAATGA 194
QY 278 leGluThrLysValVal-LysGluGluLysAlaAsnAspSerAsnPro-AsnGluGluSe 297
Db 195 TCGAAACCAAGTAGTGAAGAGGAGGAGCAATGNTAGCAACCTCGAATGAGGGATT 254
QY 297 rLys---LysThrAspLysAsnPro---GluGluSerLysSerProSerLysThr-ThrV 315
Db 255 CAAAGGAAACTGNTTAAAAACCCAGTAGNAGTTCCAGAGTNCACCAAGCAAACTTACCG 314
QY 315 al-ArgCysLeu 318
Db 315 TGTCGATGCTG 326
RESULT 11
US-08-892-880-15
; Sequence 15, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-892-880-15
Alignment Scores:
Pred. No.: 3, 35e-23 Length: 498
Score: 286.50 Matches: 62
Percent Similarity: 90.00% Conservative: 1
Best Local Similarity: 88.57% Mismatches: 4
Query Match: 17.29% Indels: 3
DB: 2 Gaps: 1
US-10-063-670-6 (1-322) x US-08-892-880-15 (1-498)
QY 254 LeuGlyPheCysTyrValLysArgTyrValLysAlaPheProPheThrAsnLysAsnGln 273
Db 14 CTTGATTTTCTATGTCAAAAGGTATGTNAAGGCTTCCTTTTACAAACAAGATCAG 73


```

; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: p-Meta-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 113...1624
US-07-946-497-1

Alignment Scores:
Pred. No.: 7,8e-15 Length: 3207
Score: 224.00 Matches: 87
Percent Similarity: 37.68% Conservative: 43
Best Local Similarity: 25.22% Mismatches: 171
Query Match: 13.52% Indels: 44
DB: 12 Gaps: 12

US-10-063-670-6 (1-322) x US-07-946-497-1 (1-3207)

QY 3 ArgCysPheSerLeuValLeuLeuLeuThr-----SerIleTrpThr 16
Db AGATCTCTTGGTTTCATCTGTCATGACATGAGCAAGTTTGGTGGCACACAGCTTGGGA 145
QY 17 ThrArgLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 36
Db CTACTTTGGCTCTTACAGTTGAGCTGGCGACAGCAGCAGATCGATTGGAATATAACCTGC 205
QY 37 ArgIleMetGlyIleThrLeuValSerLeuLysAlaAsnGlnGlnLeuAsnPheThrGlu 56
Db CTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 265
QY 57 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 76
Db GCAGCTGACCTCTGCGAGGCTTTCACACCACCTTGCACCATGCTCAGATGGAGTTA 325
QY 77 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 96
Db GCCTTGAGAAAGGGGTTTGAAACATGACGATATGGGTTCATA--GAAGGACACGCTGTA 382
QY 97 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 116
Db ATCCGAGATGATCCACCCCAACGCTATCTGTGAGCCACCAACACAGAGGTGATATCCTC 442
QY 117 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 136
Db CTGCGATCCACACCTCCACATGATGACATATGTTCAATGCCCTCAGCTCCTCTTGA 502
QY 137 AsnSerCysIleProGluIleThrThrLysAspProIlePheAsnThrGlnThrAla 156
Db GAAGACTGT-----ACATCAGTCACAGACCTACCAATTCCTTCGATGA 547
QY 157 ThrGlnThrThrGluPheIleValSerAspSerThr---TyrSerValAlaSerProTyr 175
Db CAGTTACCAATACTATTGTCACCGTGTATGGCCCGCTACAGCAAGAAGGGCGAGTAT 607
QY 176 SerThr-----IleProAlaProThr----- 182
Db AGACACACCAAGACACATCGATGCTCAACATTTATAGATGAGATGTCAGCTGA 667
QY 183 -----ThrThrProProAla---ProAlaSerThrSerIleProArgArg 196
Db TCCACCAATTGAGAAGAGACCCCGAGAGGCTCAATTTTGCACACCGACCTTCCACTTCA 727

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197 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThr---Glu 215
 728 CAGCTACTGGAGACCGGGATGACGCTTCTTATTGGGAGACACCTTGGCCCATTTGA 787
 216 ThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGly 235
 788 ACTACTCCATGGTTTCTGCCCCACACAAACAGACCGGACCGGACCGGACCGGACCGG 847
 236 Val-----ProThrAlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAla 252
 848 ATCCATTCAAACCCAGAGTACTTCTCAGACAAACCCAGGATGATGATATAGACAGA 907
 253 GlyLeuGlyPheCysTyrValLysArgTyrValLys-----AlaPheProPheThrAsn 270
 908 AACAGCACCATGCTCATGAGAAACTGGACCCAGGAACACACGCTCTTTCATATAC 967
 271 LysAsnGlnGlnLysGluMetIleGluThrLysValLysGluLysAlaAsnAsp 290
 968 CATGAGTATCAGGATGAAGAG--GAGACCCACATGCTACAAGCACACCTGGGCAGAT 1024
 291 SerAsnProAsnGluSerLysLysThrAspLys-----AsnProGlu 305
 1025 CCTAATAGCACACAGAGAGAGCAGCTACCCAGAGGAGAGTGTGTTGAGATGAATGG 1084
 306 GluSerLysSerPro 310
 1085 CAGGGAGAGAACCCA 1099

RESULT 14
 US-08-483-322-1
 ; Sequence 1, Application US/08483322
 ; Patent No. 5760178
 ; GENERAL INFORMATION:
 ; APPLICANT: HERRLICH, Peter
 ; APPLICANT: PONTA, Helmut
 ; APPLICANT: GUENTHER, Ursula
 ; APPLICANT: MATZKU, Siegfried
 ; APPLICANT: WENZL, Achim
 ; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
 ; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
 ; NUMBER OF SEQUENCES: 8 AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington, D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,322
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/946,497
 ; FILING DATE: 09-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 16915/145
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3207 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double

; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: p-Meta-1
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 113..1624
 US-08-483-322-1

Alignment Scores:

Pred. No.: 7.8e-15 Length: 3207
 Score: 224.00 Matches: 87
 Percent Similarity: 37.68% Conservative: 43
 Best Local Similarity: 25.22% Mismatches: 171
 Query Match: 13.52% Indels: 44
 Gaps: 12

US-10-063-670-6 (1-322) x US-08-483-322-1 (1-3207)

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Qy 3 ArgCysPheSerLeuValLeuLeuThr-----SerIleTyrThr 16
Db 86 AGATCCTTTGGTTTCATCTTCGACATCATGGACAAGGTTGGTGGCACACAGCTTGGGA 145

Qy 17 ThrArgLeuValGlnGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 36
Db 146 CTACTTTGCCTCTTACAGATTGAGCGTGGCCACAGCAGCAGATCGATTTCGAATATAACCTGC 205

Qy 37 ArgIleMetGlyIleThrLeuValSerIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlu 56
Db 206 CGTTACGCGAGTGATTTCATGTGGAGAAATGGCGCTACAGTATCTCCAGACTGAA 265

Qy 57 AlalysGlnAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 76
Db 266 GCAGCTGACCTCGAGGCTTTCACACACACCTTGCACCATGGCTCAGATGAGTTA 325

Qy 77 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValVal 96
Db 326 GCCCTGAGAAAGGGTTTGAACATGCGAGGTATGGTTTCATA---GAAGGACACAGTGTA 382

Qy 97 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyr 116
Db 383 ATCCCGAGGATCCACCCACGCTATCTGTGCACGCCAACACACAGGAGTGTATATCTC 442

Qy 117 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThr 136
Db 443 CTCGCATCCACACCTCCCACTATGACACATATGCTTCATGCTCAGCTCCTCTTGA 502

Qy 137 AsnSerCysIleProGluIleThrThrLysAspProIlePheAsnThrGlnThrAla 156
Db 503 GAAGACTGT-----ACATCAGTCACAGACCTACCCAAATTCCTTCGATGGA 547

Qy 157 ThrGlnThrThrGluPheIleValSerAspSerThr---TyrSerValAlaSerProTyr 175
Db 548 CCAGTTACCAATACTATTGCAACCGTGATGGCCCGCTACAGCAAGAGGGCGAGTAT 607

Qy 176 SerThr-----IleProAlaProThr----- 182
Db 608 AGAACACACCAAGAGACATCGATCGCTCAACATATATAGATGAGGATGTCAGCAGTGA 667

Qy 183 -----ThrThrProAla---ProAlaSerThrSerIleProArgArg 196
Db 668 TCCACCAATTGAGAGAGACCCAGAGAGGCTTACATTTTGGCACACCGACCTTCCCACTTCA 727

Qy 197 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThr---Glu 215
Db 728 CAGCCTACTGGAGACGGGATGACGCCCTTCTTATTTGGGAGCACCCCTGGCCACCATTTGCA 787

Qy 216 ThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGly 235
Db 788 ACTACTCCATGGGTTCTGCCCAACACAAACAGAACACCGAACGACCCAGTGGAAACCG 847

Qy 236 Val-----ProThrAlaLeuValLeuAlaLeuLeuPhePheGlyValAlaAla 252
Db 848 ATCCATTAAACCCAGAGTACTACTCAGACAAACCCACGAGATGATGATATAGACAGA 907
  
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Qy 253 GlyLeuGlyPheCysTyrValLysArgTyrValLys-----AlaPheProPheThrAsn 270
Db 308 AACAGACACCAAGTGTCTATGAGAAACTGACCCAGGACACACAGCCTCTTTCATATAC 967

Qy 271 LysAsnGlnGlnLysGluMetIleGluThrLysValValLysGluGluLysAlaAsnAsp 290
Db 968 CATGAGTATCAGGATGAAGAG---GAGACCCCATGCTACAGCACACCTGGGCAGAT 1024

Qy 291 SerAsnProAsnGluGluSerLysThrAspLys-----AsnProGlu 305
Db 1025 CCTAATAGCAACAAGAAAGACAGCTACCCAGGAGGAGAGTGTGTTGAGATGAATGG 1084

Qy 306 GluSerLysSerPro 310
Db 1085 CAGGGGAAGAACCA 1099
  
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RESULT 15

US-08-478-882-1
 ; Sequence 1, Application US/08478882
 ; Patent No. 5885575
 ; GENERAL INFORMATION:
 ; APPLICANT: HERKLICH, Peter
 ; APPLICANT: PONTA, Helmut
 ; APPLICANT: GUENTHER, Ursula
 ; APPLICANT: MATZKU, Siegfried
 ; APPLICANT: WENZL, Achim
 ; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
 ; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
 ; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington, D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/478,882
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/946,497
 ; FILING DATE: 19921109
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 16915/145
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3207 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: p-Meta-1
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 113..1624
 US-08-478-882-1

Alignment Scores: 7.8e-15 Length: 3207
 Pred. No.: 224.00 Matches: 87
 Score:

